Rec'd POS/PTO 27 SEP 200/

CRYSTAL STRUCTURE OF THE LIGAND BINDING DOMAIN OT THE RETINOIC ACID-RELATED ORPHAN RECEPTOR ALPHA (ROR-ALPHA)

FIELD OF THE INVENTION

The present invention relates ROR α in crystallized form and methods for the preparation thereof. The invention further provides a three-dimensional model of ROR α and means for the design of ROR α modulators.

BACKGROUND OF THE INVENTION

The retinoic acid-related orphan receptor α (ROR α) is an orphan member of nuclear receptor protein family to which belong receptors such as retinoic acid receptor (RAR), peroxisome proliferator-activated receptor (PPAR), estrogen receptor (ER), vitamin D receptor (VDR) and thyroid receptor (TR). Like other members of the nuclear receptor family, ROR α exhibits a modular structure composed of several domains, among them a DNA-binding domain (DBD) and a ligand-binding domain (LBD). The latter displays low degree of homology with the LBD of T3R β (25%), VDR (24%), RAR α (24%), PPAR α (24%) and RXR α (20%) from which X-ray structures have been solved. However, attempts to crystallize the LBD of ROR α have failed so far and no X-ray structure of ROR α was available. In addition, to this point, no ligand has been identified until now. Our understanding of the physiological role of the receptor would be greatly enhanced by the discovery of a natural ligand. Further, provision of the spatial organization would assist in the designing of agonists and antagonists of ROR α .

SUMMARY OF THE INVENTION

In one aspect, the present invention provides crystalline LBD of ROR α . In a related aspect the invention provides crystalline LBD of ROR α associated with a ligand.

In another aspect, the invention provides a set of co-ordinates representing the spatial organization of the LBD of ROR α . In a related aspect the invention provides a model of the LBD of ROR α comprising a set of co-ordinates embodying the structure of the LBD of ROR α . In another related aspect, this invention provides for a set of co-ordinates useful in drug design. In yet another related aspect, the invention provides for a method for identifying a substance binding to the LBD of ROR α , comprising providing a model embodying the structure of the LBD of ROR α , assessing the interaction of a candidate substance with said model, and selecting a substance which is predicted to interact with the LBD of ROR α . Substances identified by this method are also provided.

In a further aspect, the invention provides for a method for identifying a compound acting as agonist or antagonist of ROR α that binds to the LBD of ROR α comprising selecting a potential compound by performing rational drug design with one or more sets of atomic coordinates embodying the structure of the LBD of ROR α , contacting the potential compound with a LBD of ROR α and measuring the binding of the compound to the LBD of ROR α . Agonists and antagonists identified by this method are also provided.

In another aspect, the present invention provides for a method of screening for compounds interacting with ROR α comprising contacting ROR α with a candidate compound, measuring interactions between the candidate compound and ROR α in the absence of sterols, and selecting said compound if it interacts with ROR α in the absence of sterols. Preferred sterols are cholesterol or cholesterol derivatives. Compounds identified by this method are also provided.

In another aspect of the present invention, the use of ROR α for the screening of cholesterol related diseases is provided.

In yet another aspect the present invention provides a composition comprising LBD of RORα and a sterol, preferably cholesterol or a cholesterol derivative. In a preferred embodiment, said composition is crystallizable.

BRIEF DESCRIPTION OF THE TABLES AND FIGURES

- Table 1: Native crystal data and X-ray data statistics of LBD of RORα in complex with cholesterol.
- Table 2: Hg-derivative crystal data, X-ray data and heavy atom refinement statistics (for complex with cholesterol).
- Table 3: Refinement statistics (for complex with cholesterol).
- Table 4: shows effects of mutations preventing binding of cholesterol to RORa.
- Table 5: shows effects of fluvastatin on RORa transcriptional activity.
- Table 6: Effect of cholesterol and cholesterol derivative on ROR alpha transcriptional activity.
- Table 7: Native crystal data and refinement statistics of LBD of RORα in complex with cholesterol sulfate.
- Table 8: Atomic structure coordinates for a representative structure of the LBD of RORα in complex with cholesterol (numbering according to Swissprot P35398-1).
- Table 9: Atomic structure coordinates for a representative structure of the LBD of RORα in complex with cholesterol-sulfate (numbering according to Swissprot P35398-2).
- Figure 1: Sequence of human RORα (Swissprot P35398-1).

Figure 2 shows a schematic representation of the X-ray structure of the complex between RORα-LBD and cholesterol.

Figure 3 shows a zoomed in view of the complex between RORα-LBD and cholesterol (numbering according to Swissprot P35398-1).

Figure 4: Proposal of ligands in order to increase the affinity and to obtain antagonistic activity (numbering according to Swissprot P35398-1)..

Figure 5: Proposal of further derivatives of cholesterol in order to increase the affinity (numbering according to Swissprot P35398-1)..

Figure 6 shows the displacement of cholesterol by 25-OH cholesterol and cholesterol sulfate.

Figure 7 shows a zoomed view of X-ray structure of ROR(alpha)/cholesterol (numbering according to Swissprot P35398-2)..

Figure 8 Overview of interactions made by cholesterol-sulfate with LBP of ROR(alpha) (numbering according to Swissprot P35398-2)..

Figure 9 Comparison of the X-ray structures of ROR(alpha)/cholesterol-sulfate and ROR(alpha)/cholesterol (numbering according to Swissprot P35398-2).

Figure 10 Comparison of the X-ray structures of ROR(alpha)/cholesterol (left) and ROR(alpha)/cholesterol-sulfate (right) (numbering according to Swissprot P35398-2).

Figure 11 Sequence of the construct used in crystallization. The secondary structure elements are shown below the sequence. Amino acids that have a nonhydrogen atom closer than 4Å to cholesterol are highlighted in red (numbering according to Swissprot P35398-2).

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides crystals of the LBD of RORα. Moreover, the present invention provides the structural determination of such crystals by X-ray crystallography. In one embodiment, the structure of the crystal has been solved to a resolution of 1.88Å. Surprisingly, it was found that the crystal contained a ligand associated to RORα. The ligand was identified as cholest-5-en-3beta-ol (cholesterol). Thus the present invention not only provides information on the spatial organization of the LBD of RORα useful for instance for in-silico screening, docking and rational drug design, but also cholesterol as a ligand binding to the RORα which is useful for the identification of amino acids involved in the ligand binding. The information provided in accordance with the present invention can be used as basis for the design of compounds binding to the LBD of RORα, as exemplified below. The crystal LBD of RORα provided by this invention can take any crystalline form, but is preferably a single crystal. In a more preferred embodiment the crystal comprises a unit cell having the

of a=55 Å \pm 5 Å, b=50 Å \pm 5 Å, c=60 Å \pm 6 Å and β =98.5° \pm 9° and space group P2₁. Preferably, the unit cell dimensions are a=55.9 Å \pm 2 Å, b=49.9 Å \pm 2 Å, c=60.7 Å \pm 2 Å and β =98.7° \pm 5° or a=54.4ű 2 Å, b=49.9ű 2 Å, c=60.7ű 2 Å, β =97.8°± 5°. In another preferred embodiment, the crystalline LBD of RORa is of human origin. The crystalline LBD of RORa according to the present invention is preferably associated with a second chemical substance. Such a substance may be any natural or synthetic chemical molecule, preferred are small molecules, more preferred are small lipophilic molecules. Cholesterol has been identified, in accordance with the present invention, as a ligand fitting into this binding pocket. Thus, in a particularly preferred embodiment such a substance is cholesterol or a cholesterol derivative. As used herein, the term "small molecule" refers to a natural or synthetic compound, preferably an organic molecule, with a molecular weight less than 3000 Da, more preferably less than 1000 Da, most preferably less than 500 Da. The term "lipophilic", as used herein, refers to compounds that are mainly unpolar and that are not or only slightly soluble in water. Typical examples may include fatty acids, retinoic acids, melatonin, steroid hormones, vitamin D derivatives. Other examples may include lipophilic molecules like tamoxifen or raloxifen. In accordance with the present invention, a particularly preferred lipophilic ligand is cholesterol and derivatives thereof. As used herein the term "cholesterol derivative" means a molecule that possesses similarity to cholesterol, such as the same overall structure, but with different substituents or differences in the location of unsaturated bonds or sterical isomers. Examples for such cholesterol derivatives can for instance be found in http://www.steraloids.com.

Crystals of the LBD of ROR α and, optionally a second chemical species can be grown by a number of techniques including batch crystallization, vapor diffusion (either by sitting drop or hanging drop) and by microdialysis. Seeding of the crystals in some instances is required to obtain X-ray quality crystals. Standard micro and/or macro seeding of crystals may therefore be used. An initial crystal can be allowed to grow over several weeksat 4° C or at room temperature (ca. 20° C) from a hanging drop. Crystals then can be subsequently grown by macroseeding from the initial crystal. Once a crystal of the present invention is grown, X-ray diffraction data can be collected. A MAR imaging plate detector for X- ray diffraction data collection can be used for example. Crystals can be characterized by using X-rays produced in a conventional source (such as a sealed tube or a rotating anode) or using a synchrotron source.

Methods of characterization and data collection include, but are not limited to, precession photography, oscillation/rotation data collection and diffractometer data collection. As exemplified below, heavy atom derivatives can be obtained by soaking crystals in solution with 4 mM methylmercuric acetate for 1 hour. Data processing and reduction can be carried out using programs

(DENZO, and SCALEPACK) of the HKL-suite [Otwinowski and Minor, Meth. Enzymol. 276:307-326 (1997)]. Heavy atom positions can be found using programs such as SnB [Weeks, C.M. & Miller, R. (1999) J.Appl.Cryst.32, 120-124.] or programs (e.g. SHELX and RSPS) of the CCP4 program suite [Collaborative Computational Project, Number4, Acta Cryst. D53: 760-763 (1994)]. Electron density maps can be calculated using programs (e.g. MLPHARE and DM) of the CCP4 program suite [Collaborative Computational Project, Number4, Acta Cryst. D53: 760-763 (1994)] or alternatively using SHARP [La Fortelle, E. D. and Bricogne, G., Methods in Enzymology 276:472-494 1997)] and SOLOMON. Molecular models can be built into this map using O [Jones, T. a. et al., ACTA Crystallogr. A47:110-119 (1991)]. A complete molecular model for the protein can be built on the basis of the experimental electron density map. Model building interspersed with positional and simulated annealing refinement using X-PLOR, [Brunger, X-PLOR v.3.1 Manual, New Haven: Yale University, (1993)] or with CNS, using a maximum likelihood residual [Brunger, A. T. et al., Acta Cryst. D54: 905-921 (1998)] can permit an unambiguous trace and sequence assignment of the LBD of RORα.

Accordingly, the present invention provides for a model of the structure of the LBD of RORa useful for rational drug design comprising a set of co-ordinates embodying the structure of the LBD of RORa. Thus, a preferred embodiment provides for a model embodying the structure of the LBD RORa comprising one or more sets of atomic coordinates in Table 8 or 9. Other preferred embodiments provide a computer system comprising computer hardware or the model of the present invention and a computer readable medium comprising the model of the present invention. The set of co-ordinates is preferably determined by crystallographic analysis of the LBD of RORa, however any available method may be used to construct such a model using data disclosed herein or obtained from independent crystallographic analysis of the LBD of RORa. The term "structure co-ordinates" refers to Cartesian co-ordinates derived from mathematical equations related to the patterns obtained on diffraction of a monochromatic beam of X-rays by the atoms (scattering centers) of a protein or protein-ligand complex in crystal form. The diffraction data are used to calculate an electron density map of the repeating unit of the crystal. The electron density maps are then used to establish the positions of the individual atoms of the enzyme or enzyme complex. Variations in co-ordinates may be generated because of mathematical manipulations of the structure co-ordinates. For example, the structure co-ordinates set forth in Table 8 or 9 could be manipulated by crystallographic permutations of the structure co-ordinates, fractionalization of the structure co-ordinates, integer additions or subtractions to sets of the structure co-ordinates, inversion of the structure co-ordinates or any

-6-

combination of the above. Alternatively, modifications in the crystal structure due to mutations, additions, substitutions, and/or deletions of amino acids, or other changes in any of the components that make up the crystal could also account for variations in structure co-ordinates. If such variations are within an acceptable standard error as compared to the original co-ordinates, the resulting threedimensional shape is considered to be the same. Various computational analyses are therefore necessary to determine whether a molecule or molecular complex or a portion thereof is sufficiently similar to all or parts of the structure of the LBD of RORa as to be considered the same. Such analyses may be carried out in current software applications, such as the Molecular Similarity application of QUANTA (Molecular Simulations Inc., San Diego, Calif.) version 4.1, and as described in the accompanying User's Guide. For the purpose of this invention, any molecule or molecular complex that has a root mean square deviation of conserved residue backbone atoms (N, Co., C. O) of less than 1.5 Å; when superimposed on the relevant backbone atoms described by structure co-ordinates listed in Table 8 or 9 are considered identical. More preferably, the root mean square deviation is less than 1.0 Å. The term "root mean square deviation" means the square root of the arithmetic mean of the squares of the deviations from the mean. It is a way to express the deviation or variation from a trend or object. For purposes of this invention, the "root mean square deviation" defines the variation in the backbone of a protein or protein ligand complex from the relevant portion of the backbone of the LBD of RORα as defined by the structure co-ordinates described herein.

In certain embodiments, the data set embodies a portion of the structure of the LBD of RORα, including without limitation the binding pocket of LBD of RORα. The term "binding pocket", as used herein, refers to a region of a molecule or molecular complex, that, as a result of its shape, favorably associates with another chemical entity or compound. In accordance with the present invention, a preferred binding pocket includes the amino acids shown in Figures 3, 4, 5, 7, 8, 9 or 10 one or more of the following amino acids: Cys321, Gln322, Tyr323, Leu328,Trp353, Cys356, Ala357, Lys359, Ile360, Glu362, Ala363, Val397, Phe398, Arg400, Met401, Arg403, Ala404, Val412, Tyr413, Phe414, Phe424, Leu427, Cys429, Phe432, Ile433, Val436, His517, Lys520 and Tyr540 (numbering according to SWISS-PROT P35398-1).

In one embodiment of the present invention, the model may be used to identify substances that interact with the LBD of RORa. In general, molecular similarity applications in accordance with the present invention permit comparisons between different structures, different conformations of the

-7-

same structure, and different parts of the same structure. A potential interacting substance is examined through the use of computer modeling using a docking program such as GRAM, DOCK, or AUTODOCK [Dunbrack et al., Folding & Design, 2:27-42 (1997)]. This procedure can include computer fitting of potential ligands to the LBD of RORa, for example to ascertain how well the shape and the chemical structure of the potential ligand will complement with the binding pocked provided by the present application. Computer programs can also be employed to estimate the attraction, repulsion, and steric hindrance of the ligand to the LBD of RORa. Generally the tighter the fit (e.g., the lower the steric hindrance, and/or the greater the attractive force) the more potent the potential drug will be since these properties are consistent with a tighter binding constant. Furthermore, the more specificity in the design of a potential drug the more likely that the drug will not interfere with other properties of the RORa protein or other proteins (particularly proteins present in the nucleus). This will minimize potential side-effects due to unwanted interactions with other proteins. Initially a potential interacting substance could be obtained by screening a chemical library. A ligand selected in this manner could then be systematically modified by computer modeling programs until one or more promising potential ligands are identified. Alternatively, a known ligand of RORa, such as for instance cholesterol as identified in accordance with this invention, may be used as a starting point for systematic modification. Such computer modeling allows the selection of a finite number of rational chemical modifications, as opposed to the countless number of essentially random chemical modifications that could be made, and of which any one might lead to a useful drug. Each chemical modification requires additional chemical steps, which while being reasonable for the synthesis of a finite number of compounds, quickly becomes overwhelming if all possible modifications needed to be synthesized. Thus through the use of the three-dimensional structures disclosed herein and computer modeling, a large number of these compounds can be rapidly screened on the computer monitor screen, and a few likely candidates can be determined without the laborious synthesis of untold numbers of compounds.

Accordingly, methods for identifying substances that bind to the LBD of RORα are provided. Such methods typically include the steps of providing a model embodying the structure of the LBD of RORα, assessing the interaction of a candidate substance with said model, selecting a substance which is predicted to interact with the LBD of RORα, and, optionally, contacting the selected substance with the LBD of RORα. In a preferred embodiment, such a method includes comparing the 3-D structure of candidate compounds with the 3-D molecular model shown in Table 8 or 9 or with the co-ordinates of amino acids which are part of a preferred binding pocket or directly or indirectly involved in binding of a ligand, as herein disclosed for instance in Figures 3, 4, 5, 7, 8, 9 or 10.

Preferably, said amino acids can form hydrogen bonds with hydrogen bonding functional groups

(directly or via water molecules) in a candidate compound or can form favorable vdW-interactions. The interactions are preferably assessed by a computer-assisted method, such as for instance a data processing method in which the structure co-ordinate data as described above is input in a data structure such that the interatomic distances between the atoms of the LBD of $ROR\alpha$ are easily retrieved, and the distances between hydrogen-bonding functional groups of different candidate compounds and hydrogen bonding atoms of the amino acids that form the binding pocket in the 3D molecular model are compared (or the distances between groups forming vdW-interactions) thereby allowing the identification of those candidate compounds which would theoretically form the most stable complexes with the 3-D molecular model binding pocket of the LBD of RORa, based on optimal hydrogen bonding and vdW-interactions between the two structures. In a preferred embodiment the substances are designed to interact via vdW-interactions or via hydrogen bond interactions directly or indirectly (e.g. via water molecules) with atoms of one or more amino acids shown in Figures 3, 4, 5, 7, 8, 9 or 10 or selected from the group consisting of Cys321, Gln322, Tyr323, Leu328, Trp353, Cys356, Ala357, Lys359, Ile360, Glu362, Ala363, Val397, Phe398, Arg400, Met401, Arg403, Ala404, Val412, Tyr413, Phe414, Phe424, Leu427, Cys429, Phe432, Ile433, Val436, His517, Lys520 and Tyr540, Gln322, Tyr323, Arg400, Arg403. In a more preferred embodiment the substances interact via vdW-interactions or via hydrogen bond interactions directly or indirectly (e.g. via water molecules) with atoms of one or more amino acids selected from the group consisting of Gln322, Tyr323, Arg400, Arg403 or Trp353, Lys359, Ile360, Ala363, Met401, Phe414, Leu427, Phe432, Val436. Substances identified using the above methods are also provided. Preferred substances are small molecules, more preferred are small lipophilic molecules (possibly with a polar group) and particularly preferred are cholesterol or cholesterol derivatives, such as for instance cholesterol sulfate. In a further preferred embodiment, the binding constant of the substance to ROR α is at least 1 μ M, preferably at least 100nM, more preferably at least 10nM.

In addition, agonists and antagonists of ROR α are provided. In one embodiment methods for screening for agonists or antagonists of ROR α are provided. Such methods include selecting a potential agonistic or antagonistic compound by performing rational drug design with one or more sets of atomic co-ordinates embodying the structure of the LBD of ROR α , contacting the potential compound with a LBD of ROR α and measuring the biological activity of ROR α . The selection is typically made in conjunction with computer modeling. A potential compound is identified as agonist if it increases the biological activity of ROR α or as antagonist if it decreases the biological activity of

RORa. Agonists and antagonists identified by such methods are also provided. The agonist or antagonist needs not to bind to the binding pocket used by the natural ligand of RORa, but could also bind at another position and exert its effect allosterically. A preferred embodiment of an agonist according to the present invention is a compound that stabilizes helix 12 (H12) in the agonistic position, i.e. the position in which H12, together with the H3-H4 region, forms the proper interaction surface, i.e. the complete AF-2, for the coactivator (reviewed e.g. in Renaud & Moras, Cell. Mol. Life Sci., 57, 1748-1769, 2000). A preferred embodiment of an antagonist according to the present invention is a compound that destabilizes the agonistic position of H12 for instance by tilting the position of H12 (reviewed e.g. in Renaud & Moras, 2000, supra). Destabilisation of H12 may for instance be achieved by a cholesterol derivative with a bulky substituent at position 26 thus displacing Tyr540 and / or His517. In a preferred embodiment such agonists or antagonists are small molecules. Particularly preferred are lipophilic small molecules. Examples without being limiting are for instance fatty acids, retinoic acids, melatonin, steroid hormones, vitamin D derivatives, but also compounds similar to tamoxifen or raloxifen or derivatives thereof. In one embodiment, such agonists or antagonists may be cholesterol or cholesterol derivatives. In a preferred embodiment of this invention the cholesterol ligand has been modified using the structural information provided by the present invention to a cholesterol derivative binding more strongly to the ligand binding pocked (LBP) of the LBD of RORa provided by the present invention. An example for a more strongly, competitively binding cholesterol derivative that has been designed using the structural information provided by this invention is cholesterol sulfate (see below). In another preferred embodiment, the present invention provides a pharmaceutical composition comprising a therapeutically effective amount of a compound stabilizing H12 of RORa in an agonistic position and a pharmaceutically acceptable carrier. In a related embodiment, the present invention provides a pharmaceutical composition comprising a therapeutically effective amount of a compound destabilizing H12 of RORa in an agonistic position and a pharmaceutically acceptable carrier.

Once a potentially binding substance, such as an agonist or antagonist, is identified it can be either selected from a library of chemicals or alternatively the potential ligand may be synthesized de novo. The de novo synthesis of one or even a relatively small group of specific compounds is reasonable in the art of drug design. The prospective drug can be placed into any standard binding assay to test its effect on any particular ROR α function, for instance on the DNA binding of ROR α exemplified below. When a suitable drug is identified, a supplemental crystal can be grown which comprises a protein-ligand complex, for instance formed between the binding pocket of the LBD of ROR α and the

- 10 -

drug. Preferably the crystal effectively diffracts X-rays allowing the determination of the atomic coordinates of the protein-ligand complex to a resolution of greater than 5.0 Angstroms, more preferably greater than 3.0 Angstroms or greater than 2.0 Angstroms. The three-dimensional structure of the supplemental crystal can be determined by molecular replacement analysis. Molecular replacement involves using a known three-dimensional structure as a search model to determine the structure of a closely related molecule or protein-ligand complex in a new crystal form. The measured X-ray diffraction properties of the new crystal are compared with the search model structure to compute the position and orientation of the protein in the new crystal. Computer programs that can be used include: programs (AMORE, MOLREP) of the CCP4 program suite [Collaborative Computational Project, Number4, Acta Cryst. D53: 760-763 (1994)] or X-PLOR [Brunger, X-PLOR v.3.1 Manual, New Haven: Yale University, (1993)]. Once the position and orientation are known an electron density map can be calculated using the search model to provide X-ray phases. Thereafter, the electron density is inspected for structural differences and the search model is modified to conform to the new structure. Using this approach, it will be possible to use the claimed structure to solve the three-dimensional structures of any such LBD of RORa complex. For all of the drug screening assays described herein further refinements to the structure of the drug will generally be necessary and can be made by the successive iterations of any and/or all of the steps provided by the particular drug screening assay.

The substances identified by rational design can be further analyzed in drug screening assay. The drug screening assays of the present invention may use any of a number of assays for measuring the functionality of RORα, including for the ability of RORα following ligand binding to transcriptionally regulate a gene, by increasing phosphorylation of RORα, by allowing RORα to dimerize or to heterodimerize with another nuclear receptor, by improving its ability to interact with co-activators, by changing its conformation and by increasing its ability to bind DNA. In one binding assay, a nucleic acid containing a RORα binding site is placed on a coated or onto a solid support. A preferred binding site is a response element (RORE) composed of a 6 bp AT rich motif immediately preceding a half site AGGTCA and the possible variants of this response element that are given in Giguere et al. 1994, Genes & Development 8:538-553, Mc Broom et al. 1995 Mol.Cell. Biol. 15: 796 -808, Moraitis & Giguere, 1999; Molecular Endocrinology. 13:431-439. Methods for placing the nucleic acid on the solid support are well known in the art and include linking biotin to the nucleic acid and linking avidin to the solid support. The RORα is allowed to equilibrate with the nucleic acid and drugs are tested to see if they disrupt or enhance the binding.

In another assay, a co-activator protein, such as for instance GRIP or DRIP 205 (Brandon-Atkins et al. 1999, Molecular Endocrinology 13: 1550-1557), or SRC1, NcoA-1, ERAP / P160, SRC2 / NcoA-2, ACTR, SRC-3, pCIP, ERAP -140, RIP 140, RIP 160 P/Caf, CBP/P), ARA70, Ada 3, Rap 46, GRIP170, TRIP 1, PGC1 and 2, SPT6, TIF0, SW1/SNUERF, TRAP 100, TRAP 220, DRIP, NSD1 (Robyr et al. 2000, Mol. Endo. 14: 329-347), are placed on a coated or onto a solid support. The $ROR\alpha$ protein may be labeled. For example, in one embodiment radiolabeled $ROR\alpha$ proteins are used to measure the effect of a drug on binding. In another embodiment the natural ultraviolet absorbance of the RORa protein is used. In yet another embodiment, a Biacore chip (Pharmacia) coated with the co-activator peptide is used and the change in surface conductivity can be measured. In yet another embodiment, the effect of a prospective drug (a candidate compound) on interactions between RORa and their DNA binding sites are assayed in living cells that contain or can be induced to contain activated RORa proteins. Cells containing a reporter gene, such as the heterologous gene for luciferase, green fluorescent protein, chloramphenicol acetyl transferase or 3-galactosidase and the like are operably linked to a promoter containing a $ROR\alpha$ binding site. A prospective drug is then contacted with the cell. The amount (and/or activity) of reporter produced in the absence and presence of prospective drug is determined and compared. Prospective drugs which reduce the amount (and/or activity) of reporter produced are candidate antagonists of the RORa DNA binding, whereas prospective drugs which increase the amount (and/or activity) of reporter produced are candidate agonists of RORa DNA binding. Assays for detecting the reporter gene products are readily available in the literature. For example, luciferase assays can be performed according to the manufacturer's protocol (Promega), and beta-galactosidase assays can be performed as described by Ausubel et al., [in Current Protocols in Molecular Biology, J. Wiley & Sons, Inc. (1994)]. In one example, the transfection reaction can comprise the transfection of a cell with a plasmid modified to contain a RORa protein.

In one embodiment, the prospective drugs identified by the methods of this invention can be tested for pharmacological activity using assays known in the art. For example, the identified prospective drugs can be tested for activity as potential drugs for the prophylaxis or treatment of a disease or medical condition which involves excessive bone or cartilage loss using a method as disclosed in WO 01/26737. For instance, a reporter assay can be carried out using the bone sialoprotein (BSP) or osteocalcin (OC), which are known modulators of bone mineralization and remodelling. Suitable cells can be transfected with a reporter construct in which a BSP or an OC promoter drive a reporter gene, such as the firefly luciferase gene. A prospective drug is then contacted with the cell. The amount of

- 12 -

luciferase activity produced in the absence and presence of prospective drug is determined and compared. In another embodiment, the system for testing prospective drugs according to the present invention can be the use of classical ovariectomized rat model, the loss of ovarian function induces a drop in circulating estrogen promptly followed by decrease of bone mass (Wronski et al., Calcified Tissue International. 45(6):360, 1989). The drug will be tested on ovariectomized animal for a curative treatment of 8 weeks started twelve weeks after ovariectomy and bone mineral density will be monitored. Another type of experiment could be envisaged which is a preventive treatment of intact animals for eight weeks.

Cholesterol has been found to be a ligand of RORa. In accordance with this finding, the present invention provides novel assay methods for the identification of compounds binding to RORa, in particular for the identification of compounds modulating $ROR\alpha$ activity, wherein interactions between the candidate compounds and RORa are allowed to take place in a surrounding reduced in cholesterol, preferably free of cholesterol. Such a method typically includes the steps of (a) contacting RORα with a candidate compound, (b) measuring interactions between the candidate compound and RORa in a surrounding essentially free of cholesterol, and (c) selecting said compound if it interacts with RORa. Though not a requirement, it is preferred that all method-steps are carried out in the cholesterol-reduced, or preferably essentially cholesterol-free, surrounding. In a more preferred embodiment, such a method relates to a eukaryotic cellular system. In a yet even more preferred embodiment insect cells are used. Insect cells differ from eukaryotic cells by lacking the capacity for de novo sterol synthesis. It has been shown that these cells can be propagated under cholesterol-free conditions (Cleverley et al. 1997, Exp. Cell Res. 233: 288-296). Thus, such a cell system could for instance provide an appropriate cell background to monitor the activity of a RORa ligand using the RORα cloned in an appropriate insect cell vector and the classical reporter ROREtkluc. In another embodiment, eukaryotic cells, preferably human cells, are used. These cells can for instance be cultured in medium essentially free of cholesterol and in serum essentially free of LDL- cholesterol (the LDL - free serum preparation is described in Goldstein et al 1983, Methods in Enzymology 98:241-260). Mammalian cells are able to produce cholesterol endogenously. The meaning of essentially cholesterol-free surrounding according to the present invention does not include such endogenously produced cholesterol. In a particular embodiment, endogenously cholesterol producing mammalian cells could for instance be used in an assay to screen the ability of a compound to displace endogenous cholesterol.

Nuclear receptors are known to regulate the transcription of specific genes or sets of genes upon ligand binding, which makes them interesting targets for the screening for compounds useful as therapeutics. So far, however, deeper understanding of the molecular mechanism of RORα that could lead to development of therapeutics has been severely hampered by the lack of knowledge of a ligand that binds the LBD of RORα. The identification of cholesterol as ligand of the receptor RORα in accordance with the present invention, now provides new insights into the physiological role of RORα and provides RORα as a target for the screening for compounds useful for the treatment of cholesterol related-diseases. It has been shown that defects in cholesterol biosynthesis lead to a variety of clinical characteristics (Nwokoro et al., Mol Genet Metab 74:1-2 105-19 2001), covering brain damage, skeletal defects, with in some cases osteosclerosis, limb aplasia or vetebral hypoplasia. Thus, cholesterol related diseases may include endocrine disorders, atherosclerosis and cardiovascular diseases, metabolic diseases such as for instance obesity, inflammatory diseases, skin diseases, diseases related to the CNS, such as for instance Alzheimer disease and disorders in cell proliferation and apoptosis such as tumor related diseases.

In one embodiment, the present invention provides ROR α as target for the screening of compounds useful for the treatment of endocrine disorders, in particular disorders that are related to the synthesis of steroid hormones or the regulation of steroidogenesis. In all steroidogenic tissues, regardless of the hormones synthesized, the initial step in steroidogenic cells is the conversion of cholesterol to the first steroid, pregnenolone (Stocco, Ann Rev Physiol 63: 193-213; 2001).

In another embodiment, the present invention provides ROR α as target for the screening of compounds useful for the treatment of disorders of the cholesterol homeostasis. Breakdown of cholesterol homeostasis causes disease states, the most common being atherosclerosis. Hypercholesterolemia is a well-known risk factor. Using statins the present inventions shows a direct link between the activity of ROR α and a potent anti-atherosclerosis molecule (Table 5) demonstrating the usefulness of ROR α as molecular target for the search of compounds to fight atherosclerosis and cardiovascular diseases.

In another embodiment, the present invention provides ROR α as target for the screening of compounds useful for the treatment of metabolic disorders. It is known that a cascade of events initiates adipogenesis where C/EBP and PPAR γ are important players. Furthermore, ROR α is able to strongly induce PPAR γ (Sundvold et al. Biochem. Biophys. Res. Com. 287: 383-390; 2001). SREBP

promotes the adipogenic program and SREBP activity is sensitive to the level of intracellular cholesterol (Brown et al. Cell 89: 331-340,1997). Thus, in accordance with this invention, ROR α is provided as a target for the screening of compounds useful for the treatment of disorders related to adipogenesis, development of obesity and insulin resistance, which can lead to type 2 diabetes. Furthermore, the mature adipocytes secrete factors that play a role in immunological responses, vascular disease and appetite regulation. Adipocytes derived factors include leptin, prostaglandin's and resistin. The present invention providing cholesterol as ligand of ROR α thus provide ROR α as target for screening for compounds useful for the treatment of diseases related to immune response, vascular disease and appetite regulation.

It has recently been shown that mesenchymal stem cells have the potential to differentiate into these three lineage (Pittenger et al., 1999 Science 284:143-147). Thus, an apparent reciprocal relationship is postulated to exist between the adipocyte and osteoblast phenotypes. This balance is switched toward adipocytes in osteoporotic patients. This invention provides ROR α (as PPAR γ or C/EBP) as important players in the adipogenesis pathway or in the differentiation of mesenchymal stem cells into adipocytic, chondrocytic or osteoblastic lineage. Thus, the present invention links ROR α in this switch toward adipogenesis and therefore is a potential target for therapeutic intervention in osteoporosis.

In another embodiment, the present invention provides ROR α as target for the screening of compounds useful for the treatment of inflammatory diseases. Molecular links have been established between cholesterol and cytokines showing the involvement of inflammation and immunity in atherogenesis. In addition, ROR α is involved in inflammation (WO01/26737, Bourdji et al. J. Biol Chem.275: 12243-12250 2000, Delerive et al., EMBO reports 21: 42-48; 2001).

In another embodiment, the present invention provides ROR α as target for the screening of compounds useful for the treatment of skin disorders. ROR α is highly expressed in skin (Becker-Andre, 1993; Biochem. Biophys. Res. Commun. 194:1371-1379). In addition, clinical observation of patients with genetic disorders of cholesterol biosynthesis report photosensitivity and patchy alopecia, as well as follicular atrophoderma.

In another embodiment, the present invention provides ROR α as target for the screening of compounds useful for the treatment of Alzheimer disease. The lipoprotein allele ApoE4 is associated with an increased incidence of Alzheimer disease (Trittmatter et al. Proc. Natl. Acad. Sci.USA 90:

1977-1981; 1993); the depletion of plasma membrane cholesterol in hippocampal neurons inhibits the formation of Abeta (Simons et al. PNAS 95: 6460-6464;1998), the cleavage product of the amyloid precursor protein, that is a key factor in the pathogenesis of the disease. In addition the main characteristics of the RORa knock out mice is a severe ataxia and their cerebellum is markedly atrophied. This is implicated in rare inherited disease where people are subject to movement disorders.

A DNA fragment encoding part of polyhedrin promoter up to the ATG codon is amplified by PCR

EXAMPLES

called pXI338.

Cloning and expression of (His)₆RORα-LBD304-556

from the pBAKPac8 plasmid (Clontech) by using the oligonucleotide RS365 (5'-ACCATCTCGCAAATAAATAAG-3') and MG384 (5'-ATGATGATGATGATGATGCC-TGCTGCCCATGGTGGGAACTCGAGGCCTGCAGGG-3'). MG384 has a 5'extension not present on the template DNA but which is encoding for a Kozak sequence in front of the ATG codon and part of the His tag which will be present in the final engineered vector. The second PCR reaction is run with the oligonucleotides MG383 (5'-GCCATCATCATCATCATC-ATCTGGAAGTTCTGTTCCAGGGGCCCGCAGAATTAGAACACCTTGC-3') and MG385 (5'-GTACCAGATCTTCTAGATTCGTTACCCATCAATTTGCATTG-3') on a plasmid template encoding the ligand binding domain (aa304 to aa 556; numbering according to SWISS-PROT P35398-1) of the RORa protein. As for the first PCR fragment, the oligonucleotide MG383 has a 5'extension complementing the extension present on the first PCR fragment and which is added by the extension of the fragment by MG384. By mixing both new fragments and with an PCR amplification with MG365 and RS365 a new fragment encoding the Kozak sequence, the ATG, the (His)6-tag and the cleavage site for the PreScission protease cleavage site (AmershamPharmacia) is introduced in front of the RORa ligand binding domain. This new fragment has at the both end two homology regions en common with the target plasmid pBAKPac8. The integration of the engineered gene into the cloning vector is done by using the method we described earlier (Geiser et al, BioTechniques 31 88-92,2001). DNA sequence analysis of the resulting clones confirms that the clone is as intended. The plasmid is

The plasmid pX1338 is co-transfected with linearised BacPAK6 (AcNPV) virus DNA into Sf-21 insect cells using lipofection. The viral supernatant harvested after five days is subjected to plaque purification to obtain homogenous virus populations, which are subsequently amplified on small scale and analyzed for production by Western blotting. A band of correct size is readily detectable using an

anti-RORα antibody (Santa Cruz, Cat.No. sc-6062) in all six analyzed cell pellets. One viral isolate is chosen for further amplification; a master virus stock, followed by a working virus stock are generated by further amplification in Sf-9 cells; titers are determined by plaque assay. A kinetic experiment reveals optimal production conditions for RORα-sLBD using 1 MOI at 1.82 x 106 cells/ml (TOI) for 72 hours. Under these conditions a large fraction of the protein remained soluble in the insect cells. Two Wave Bioreactor runs are performed of approx. 10-13 liters each under the above described conditions. Cells are harvested by centrifugation for 10 minutes at 6000 g in a Heraeus Cryofuge M7000, and the pellets are stored at -80° C.

Purification and characterization of (His)₆RORα-LBD304-556

(His)₆RORα-LBD₃₀₄₋₅₅₆ is purified by Ni-NTA chromatography followed by anion-exchange and size exclusion chromatography according to standard methods. From 20-g cell paste, around 15 mg of (His)₆RORα-LBD₃₀₄₋₅₅₆ is purified. The protein runs as a monomer on the size exclusion chromatography. N-terminal sequence analysis shows that the N-terminus is blocked. Mass spectrometry analysis shows a homogeneous molecular mass of 31'515.4 corresponding to Acetyl-desMet-(His)₆RORα-LBD₃₀₄₋₅₅₆ (Acet-GSSHHHHHHHLEVLFQGPAELEH...MQIDG). Proteolytic cleavage of the N-terminal 6xHis tag by the PreScissionTM protease results in a homogeneous protein that however does not yield useful crystals. In contrast, uncleaved RORα-LBD leads to crystals suitable for X-ray diffraction analysis.

Crystallization

Recombinant human ROR α -LBD in 50 mM Tris-HCl pH 7.5, 100 mM NaCl, 5 mM DTT is concentrated to 14 mg/ml. Crystallization is performed using a standard vapor diffusion hanging drop set-up, with VDX crystallization plates and siliconized microscope cover slips from Hampton Research. Crystallization droplets are made by mixing on the coverslips 2.0 μ l of the protein stock solution with 2.0 μ l of reservoir solution and equilibrated against 700 μ l of reservoir solution at 20°C. Commercially available screening kits are used to find preliminary crystallization conditions. In the refined conditions, crystals grow within 2 weeks at 20°C to a size of 0.15x 0.15 x 0.3 mm with a reservoir of 100 mM Tris-HCl pH 8.4, 19% PEG 6000, 0.2M CaCl₂. The space group of the native crystals is P21, with unit cell parameters a = 55.9 Å, b = 49.9 Å, c = 60.7 Å, $b = 98.7^{\circ}$ and space group P2₁. There is one monomer per asymmetric unit. The crystals diffract at the synchrotron (SNBL at ESRF, Grenoble) to at least 1.88 Å.

X-ray data collection

For the native data collection, a crystal grown as described above is transferred to 5µl of solution containing 20% glycerol (in addition to the reservoir composition) for about 10 seconds. The crystal is then rapidly mounted in a nylon CryoLoop (Hampton Research) and directly frozen in a cold nitrogen stream for X-ray data collection at 105K. Diffraction data are collected with the mar345 image plate system of the Swiss-Norwegian beamline of the European Synchrotron Radiation Facility (λ=0.8727Å). A total of 230 images of 1.0° rotation each are collected in time mode (15sec per frame) with a crystal-to-detector distance of 178mm (using a readout plate-diameter of 180mm). Raw diffraction data are processed and scaled with the HKL program suite version 1.96.6 (Otwinowski and Minor, 1996). Crystal data and data collection statistics for the native data are shown in Table 4. The space group of the native crystals is P2₁, with unit cell parameters a = 55.9 Å, b = 49.9 Å, c = 60.7 Å, $\beta = 98.7^{\circ}$. There is one monomer per asymmetric unit. The estimated B-factor by Wilson plot is 30 Å². For the Hg-derivative data collection, a crystal is soaked previously for 1hr in 5µl of solution containing 4mM methylmercuric acetate (in addition to the reservoir composition). Cryocooling is then done as for the native crystal. Diffraction data are collected with the mar345 image plate system of the Swiss-Norwegian beamline of the European Synchrotron Radiation Facility (λ=0.8727Å). A total of 287 images of 1.0° rotation each are collected in time mode (15sec per frame) with a crystalto-detector distance of 178mm (using a readout plate-diameter of 180mm). Raw diffraction data are processed and scaled with the HKL program suite version 1.96.6 (Otwinowski and Minor, 1996). Crystal data and data collection statistics for the Hg-derivative data are shown in Table 2. The space group of the Hg-derivative crystals is P2₁, with unit cell parameters a = 55.6 Å, b = 50.0 Å, c = 60.1Å, $\beta = 98.0^{\circ}$. There is one monomer per asymmetric unit. The estimated B-factor by Wilson plot is 29 $Å^2$.

Structure solution

Attempts to solve the structure by molecular replacement with the programs AmoRe (Navaza, 1994) or MOLREP version 6.2.5. (Vagin & Teplyakov, J.Appl.Cryst. 30, 1022-1025, 1997) by using several different models based on the coordinates of the pdb-entries 2lbd (hRARγ) or 1bsx (hTRβ) are not successful. Data from a single-wavelength experiment on the mercury-substituted crystal are thus used together with a native data set for the initial phasing by SIRAS. Anomalous as well as isomorphous difference Patterson maps reveal at least one common dominant peak. SnB version 2.1 (Weeks & Miller, J.Appl.Cryst. 32, 120-124, 1999) with DREAR normalization (Blessing & Smith, J.Appl.Cryst. 32, 664-670, 1999) using the observed anomalous differences is used to determine 4 Hg-

sites. The heavy-atom parameters are subsequently refined using MLPHARE version 4.1 (CCP4, 1994). Subsequent density modification with DM (CCP4, 1994) result in an excellent experimental SIRAS-map. Skeletonization with mapman enables chain-tracing and model building with O version 7.0 (Jones *et al.*, Acta Crystallogr. A47:110-19, 1991).

Refinement

After building the protein (residues His308-Phe544 had visible electron density) and insertion of 112 water molecules into the experimental SIRAS-map, several alternate cycles of refinement and manual rebuilding result in a model with $R_{cryst} = 28.1\%$ (8Å-1.88Å), that give excellent 2Fo-Fc and Fo-Fc maps for a ligand in the LBP. The excellent quality of the electron density allows the unambiguous identification of the ligand as being cholest-5-en-3beta-ol (cholesterol). The cholesterol ligand is then built into the electron density and X-PLOR parameter- and structure-files can be generated with the program XPLO2D (Kleywegt G., CCP4/ESF-EACBM Newsletter on Protein Crystallography 31, 45-50, 1995) that can be used to generate the X-PLOR parameter- and structure-files. Further cycles of refinement and insertion of 119 more water molecules (leading to a total of 231 water molecules) yield the final $R_{cryst} = 24.8\%$ and $R_{free} = 26.3\%$ (no sigma cutoff, 8Å-1.8Å, working set of 25592 unique reflections, test set of 1279 reflections). In general, the electron density is of excellent quality, except for the loop 493-498 which has weak density (residues 308-544 are included in model). Refinement is done with X-PLOR 3.1 (A.Bruenger, X-PLOR Version 3.1: A system for X-ray Crystallography and NMR. Yale University Press, New Haven, CT, USA, 1992) using the Engh and Huber force field for the protein (Engh & Huber, Acta Crystallogr. A47:392-400, 1991). The chain identifiers used are A for the protein (residues His308-Phe544, numbering according to SWISS-PROT P35398-1), L for the ligand (cholesterol: residue 1) and V for the water molecules (total of 231). The atom numbers used for the ligand cholesterol in the pdb-file are not the same as the atom numbers according to IUPAC-IUB.

The quality of the model is assessed with X-PLOR 3.1 (A.Bruenger, id 1992) and PROCHECK v3.3 (Laskowski *et al.*, J. Appl. Cryst. 1992; 26:283-91) (see Table 3). The final model of the complex RORα/cholesterol has good geometry (rms bond lengths = 0.013Å, rms bond angles = 1.46°) and no residues are in disallowed regions of the Ramachandran plot, as determined by PROCHECK v3.3. Molecular graphics pictures are made with O version 7.0 (Jones *et al.*, id 1991).

Table 1:

Number of oractele	1
Number of crystals	P2 ₁
Space group	55.9Å, 49.9Å, 60.7Å
Unit cell dimensions	
	β=98.7°
Number of monomers / a.u.	1
Packing coefficient	$3.2\text{Å}^3/\text{Da}$
Resolution range	15.0 – 1.88Å
Number of observations	109,306
Number of rejected observations	373 (0.34%)
Number of unique reflections	26,882
Wavelength	0.8727Å
Overall	
Data redundancy	4.1
Data completeness	9 9.2%
< Ι/ σ (I)>	29.5
$R_{\text{sym}}(I)$	0.056
Reflections with $I \ge 3\sigma(I)$	75.1%
Highest resolution shell	
Resolution range	1.95-1.88Å
Completeness for shell	93.2%
R _{sym} (I) for shell	0.437
Reflections with $I \ge 3\sigma(I)$	30.5%

Table 2:

Number of crystals	1
Space group	P2 ₁
Unit cell dimensions	55.6Å, 50.0Å, 60.1Å
	β=98.0°
Number of monomers / a.u.	1
Packing coefficient	3.2Å ³ /Da
Resolution range	10.0 - 1.88Å
Number of observations	121,716
Number of rejected observations	4140 (3.4%)
Number of unique reflections	25,136
Wavelength	0.8727Å

	<u> </u>
Overall	
Data redundancy	4.8
Data completeness	93.6%
< Ι/ σ (I)>	25.3
$R_{sym}(I)$	0.057
Reflections with $I \ge 3\sigma(I)$	81.8%
Highest resolution shell	•
Resolution range	1.95-1.88Å
Completeness for shell	76.2%
$R_{\text{sym}}(I)$ for shell	0.354
Reflections with $I \ge 3\sigma(I)$	44.5%
Resolution range used for phasing	10.0-1.94Å
R _{merge} (F) between native and Hg	23.8%
No. of common reflections	23,396
Phasing power for acentric data	1.16
Phasing power for centric data	0.80
Overall figure of merit	0.314
R _{cullis} on centric zone	0.80
Heavy atom site 1 (x,y,z, occ,Bfac)	-0.373, -0.546, -0.754, 0.387, 23.9
Heavy atom site 2 (x,y,z, occ,Bfac)	-0.515, -0.611, -0.927, 0.429, 35.5
Heavy atom site 3 (x,y,z, occ,Bfac)	-0.839, -0.478, -0.700, 0.265, 29.3
Heavy atom site 4 (x,y,z, occ,Bfac)	-0.360, -0.797, -0.896, 0.270, 36.3

Table 3:

Data used in refinement	_
- resolution range	8.0-1.88Å
- intensity cutoff (σ(F))	0.0
- number of reflections (working set)	25,592
- number of reflections (test set)	1,279
- completeness (working +test set)	99.0%
Fit to data used in refinement	
- overall R _{cryst}	0.248
- overall R _{free}	0.263
Number of non-hydrogen atoms	
- protein atoms	1,953
- ligand atoms	28
- water molecules	231
Mean B values	
- mean B value for protein	38.3 Å ²
- mean B value for ligand	20.1 Å^2
- mean B value for water molecules	51.8 Å ²
Rms deviations from ideal values	
- bond lengths	0.013 Å

- bond angles	1.46°
- dihedral angles	20.3°
- improper angles	1.3°
Residues in disallowed region of Ramachandran plot	0
PROCHECK G-factor	0.28

Overall structure of the RORα-LBD

The RORa-LBD adopts the canonical fold for the NR-LBDs (Wurtz et al., Nat Struct Biol 3, 206 1996) and in addition has the two helices H2* and H11*. RORα-LBD is in an agonist-bound state, as judged by the position of H12 (see also Figures 2 and 3). H12 in this position, together with the H3-H4 region, forms the proper interaction surface, i.e. the complete AF-2, for the coactivator (reviewed in Renaud & Moras, Cell. Mol. Life Sci., 57, 1748-1769, 2000). No coactivator peptide is added in order to obtain this crystal structure. An additional H2* helix is also found between H2 and H3 for the peroxisome proliferator-activated receptors (PPARs; Nolte et al., Nature, 395, 137-143, 1998). H11* is unique to RORa-LBD (and RORB-LBD, Stehlin et al., Embo J., 20, 5822-5832, 2001) among the known LBD structures; it roughly superposes with the middle part of loop 11-12 of RAR. The overall structure of RORα-LBD is similar to the one of RORβ-LBD (e.g. as judged by Fig.4 in Stehlin et al., id 2001), but since the coordinates of RORβ-LBD are not available, no quantitative comparison with RORG-LBD can be made. For RORG-LBD, the putative entrance site (as judged by the solvent accessible surface of the complex) for the ligand is located between H2 and H3, and not on the H12side, as hypothesized e.g. for RAR-7 (Renaud et al, Nature, 378, 681-689,1995). In the crystal, the RORα-LBD molecule of the asymmetric unit does not form a dimer with a neighbouring molecule. This is consistent with the finding, that on native gels RORα-LBD behaves as a monomer. The following Cys-residues have reacted with methylmercuric acetate (c.f. table 2 for fractional coordinates of Hg-sites): Cys321 (site 3), Cys429 (site 1), Cys505 (site 4) and Cys514 (site 2). These reactive Cys-residues are thus candidates for mutations into Ser, in order to possibly obtain soluble expression in E. Coli. The protein species present in the crystallization setups correspond to the following sequences His₆-tag and PreScissionTM cleavage site and residue 304-556 of RORα-LBD: Ac-GSSHHHHHHHLEVLFOGPAELEHLA...ELFTSEFEPAMQIDG In this crystal structure, well-defined electron density is found for the subsequence residue 308-544

(numbering according to Swissprot P35398-1).

Identification of the ligand and description of the ligand binding pocket

- 22 -

A small-molecule X-ray structure of 26-OH-cholesterol from the CSD (entry FIZDUN) shows a perfect, unambigous fit (after removal of the 26-OH group and rotation of 120° around the C24-C25 bond) into this unbiased electron density. The excellent quality of the high-resolution map thus allows the identification of the ligand as being cholest-5-en-3beta-ol (cholesterol). A closer look on Ligand binding pocket of RORa shows that C27 of the terminal isopropyl-group of cholesterol makes vdWcontacts with the sidechain of Trp353, while C26 makes vdW-contacts with the sidechain of Ile360. Substituents on C26 have the potential to influence the position of H12 (e.g. bulky substituents on C26 could displace H12 from its agonist-position, thus leading to an antagonistic derivative of cholesterol). H12 in this crystal structure adopts the agonist position. It is stabilized in the agonist position by the hydrogen bond (distance 2.8Å) between OH-Tyr540 (on H12) and NE2-His517 (on H11). These two residues are conserved among the α -, β -, and γ - isotypes of ROR. The LBP is essentially hydrophobic on the AF-2 side (H5 N-terminus, H6, H7, H10, H12) with the exception of Tyr540 and His517 which form an intermolecular hydrogen bond (distance between OH-Tyr540 and NE2-His517 is 2.8Å). The LBP is more polar on the H3 side (loop 1-2, H3, H5 Cterminus). The main chain NHs of Gln322 and Tyr323 on loop 1-2 and the side chains of Arg400 and Arg403 on H5 contribute to the generation of a positive electrostatic potential. A negatively charged

Arg403 on H5 contribute to the generation of a positive electrostatic potential. A negatively charged substituent (e.g. SO₄⁻) on the 3-ol group could thus yield a derivative with considerably increased affinity (Figure 4). There are 12 well-ordered water molecules in the hydrophilic part. 5 of these water molecules are amongst the 7 water molecules (of the total of 231 water molecules) which have the lowest B-factors (14 Å²-24 Å²). The 3-ol group of cholesterol makes, via a network of well-ordered water molecules, water-mediated hydrogen bonds to NE-Arg403, NH2-Arg403, CO-Arg400, NH1-Arg400, NH-Tyr323, OE1-Gln322 and NH-Gln322.

The average B-value for the ligand (20.1 Å²) is lower than the average B-value for the protein (38.3 Å²), consistent with the fact that excellent electron density for all non-hydrogen atoms of cholesterol is visible. Cholesterol adopts thus a well defined, single conformation in the LBP. This is in contrast with the multiple low-energy conformations described for the non-natural ligand stearic acid present in the ROR β -LBD (Stehlin et al., id 2001). The following residues have a non-hydrogen atom closer than 4Å to the ligand cholesterol: Trp353, Cys356, Lys359, Ile360, Ala363, Val397, Arg400, Met401, Val412, Tyr413, Phe414, Phe424, Leu427, Phe432, Val436 and His517.

Design of cholesterol derivative binding to LBD of RORa

Overall, there is a very good fit of the ligand cholesterol to the LBP. Nevertheless, a comparison of the vdW-surface of the ligand with the vdW-surface of the LBP shows that there are still a few

possibilities for derivatizations of cholesterol (Figure 4 and 5), which could increase the affinity. Additional hydrogen bonds could be gained with hydroxy-groups added to position 6 (hydrogen bond via water to OE1-Glu362), position 19 (hydrogen bond to CO-Tyr413) or position 26 (hydrogen bond to OH-Tyr540 and/or NE2-His517). Considerable electrostatic interaction energy could be gained with a charged group, e.g. SO₄⁻, added to position 3 (hydrogen bonds and electrostatic interactions via water molecules to NH1-Arg400, NH2-Arg403, NE-Arg403, NH-Gln322 and/or to NH-Tyr323). Additional vdW-interactions could be gained by additional methyl-groups added to position 12 (vdW-contacts to the sidechains of Phe398, Met401), position 18 (vdW-contacts to the sidechains of Val412, Phe398), position 27 (vdW-contacts to the sidechains of Trp353, Cys429, Phe432) or an additional ethyl-group added to position 21 (vdW-contacts to the sidechains of Phe424, Ile433, Val436, Phe437). Modifications in positions 4 and 6 could be utilized to modify, if necessary, the physicochemical or pharmacokinetic parameters, without considerably changing the affinity. Derivatives in position 26, with a bulky substituent, would have the potential to destabilize H12 in its agonist-position, thus conferring an antagonistic activity on the derivative.

Mechanism of action for cholesterol

The present X-ray structure promotes the following structural mechanism of action: Cholesterol (or possibly a cholesterol-derivative) enters the LBP from the H2,H3-side, possibly guided by the electrostatic field generated from Arg400 and Arg403. The isopropyl-end of cholesterol (or a derivative in this position) then influences the other end of the LBP, which is in contact with H12, thus regulating the binding of a coactivator to the LXXLL-binding site. A cholesterol-derivative with a bulky substituent on C26 could displace H12 from its agonist conformation, thus preventing coactivator binding, while a cholesterol derivative which further stabilizes the hydrogen bond between Tyr540 and His517 would further enforce the agonist conformation.

Selected mutations of RORα-LBD

Using the coordinates from the RORα-LBD X-ray structure a series of point mutations in the LBP are designed which should prevent binding of cholesterol and in addition a mutation is proposed which should prevent/reduce H12-stabilization via loss of the hydrogen bond between Tyr540 (on H12) and His517 (Tyr 540 -> Phe 540 mutation). The details of the mutations are included below.

clone name	mutated amino acid	Mutated nucleic acids
SDM1-1	Cys356 -> Leu356	TGT -> TTA
SDM2-3	Ala363 -> Leu363	GCT -> CTT

PCT/EP03/04433 WO 03/093312

Ala404 -> Gln404	GCC -> CAA
Phe432 -> Trp432	TTT -> TGG
His517 -> Trp517	CAT -> TGG
Tyr540 -> Phe540	TAC -> TTC
	Phe432 -> Trp432 His517 -> Trp517

- 24 -

In a transient transfection experiment, the transcriptional activity of the RORa mutants is compared to their wild type counterpart: U2OS cells are transfected with the expression vector for RORa (ROR) or its mutated form together with a luciferase reporter gene bearing a consensus response element for RORa (RORE-tk-luc). Luciferase activity is assayed in cells from 6 well plates and related to the activity in cells transfected with the wild type RORa expression plasmid. The results are normalized to the protein content. The figure shows the mean ± SD and on the left panel the results are expressed as % of induction compared to the activity of the wild type RORa. As shown in Table 4 all mutations, in the LBP (except the mutation Phe 432->Trp 432) significantly/drastically reduce the transcriptional activity of RORa leading to the conclusion that indeed RORa in its active form is bound to cholesterol. The sidechain of the mutated Trp432 has the possibility to adopt a conformation for which no steric clash with cholesterol in the LBP occurs, if the sidechains of Arg516 and Lys 520 also accordingly change their conformations. Since the latter two residues are on the surface and their sidechain conformations are not stabilized by interactions, this provides an explanation for the only slight loss of transcriptional activity for the Phe432 -> Trp432 mutation, in contrast to the other mutations in the LBP, for which there is no alternate side-chain conformation possible which would prevent a steric clash with cholesterol. The mutation Tyr 540 -> Phe 540 leads to a ca. 40% loss in transcriptional activity, showing that the hydrogen bond between Tyr 540 and His 517 contributes in a significant amount to the stabilization of H12 in the agonist position.

Table 4:

% Activity compared to WT
33.3
18.18
8.33
90.9
10
54.54

Effects of fluvastatin, an inhibitor of HMG CoA-reductase, on RORα transcriptional activity Mammalian cells receive cholesterol by uptake from lipoproteins (LDL - cholesterol) and are able to synthesize cholesterol through the mevalonate pathway. In a situation where cells are cultured under

conditions essentially sterol free, a key transcription factor, SREBP will be proteolytically cleaved and this releases a transcription factor to the nucleus. This transcription factor is able to transcriptionally activate HMG - CoA reductase, which is a critical step in the cholesterol biosynthesis through the mevalonate pathway. Statins, which are know drugs for hypercholesterol state are specific inhibitors of the HMG - CoA reductase. When cells are cultivated in sterol free medium, their HMG - CoA reductase is strongly activated. In this experiment cells, cultivated in medium essentially sterol free, are treated with fluvastatin. A clear decrease in ROR α activity is observed, leading to the conclusion that the lowering of the intracellular cholesterol level is translated by a decrease of ROR α transcriptional activity (Table 5). U2OS cells are transfected with expression vector for ROR α (ROR) together with a luciferase reporter gene bearing a consensus response element for ROR α (RORE-tk-luc). Luciferase activity is assayed in cells from 6 well plates and related to the activity in cells transfected with or without treatment with fluvastatin. The results are normalized to the protein content.

Table 5:

Fluvastatin	Fold induction	± SEM
Control	76	14
+ 5 µM	48	7
Control	93	6
+ 10 uM	38	2

Cholesterol sulfate inhibition of RORa binding to RORE

Various cholesterol derivatives including cholesterol sulfate (cpd No. 12 in Table 6): are screened in essentially cholesterol-free medium for binding of RORα to the RORE. The RORα protein is expressed in the baculovirus system. The other compounds are: No. 2: 5α-Cholestan-3-one (Steraloids C4550), 3: 4-Cholesten-3α-ol (C6090), 4: 5-Cholesten-3β, 6-diol (C6418), 5: 5-Cholesten-3β, 7α-diol 7-benzoate (C6425), 6: 5-Cholesten-3β, 7β-diol 7-benzoate (C6438), 7: 5-Cholesten-3β, 19-diol (C6470), 8: 5-, 25R-Cholesten-3β, 26-diol (C6570), 9: 5-Cholesten-24β-ethyl-3β-ol acetate (C6681), 10: 5-Cholesten-3α-ol (C6730), 11: 5-Cholesten-3β-ol (C6760), 12: 5-Cholesten-3β-ol sulfate, sodium salt (C6905), 13: 7, (5α)-Cholesten-3β-ol (C7400), 14: 7-Dehydrocholesterol (Fluka 30800). This indicates that cholesterol sulfate, as predicted by the X-ray structure, is able to displace cholesterol.

Effect of cholesterol and cholesterol derivative on ROR alpha transcriptional activity

We next establish whether in eukaryotic cells partially depleted of cholesterol, ROR α transcriptional activity can be reconstituted by addition of cholesterol. We therefore treat the cells with

hydroxypropyl-β-cyclodextrin (HPCD), a cyclodextrin derivative known to function as a cholesterol shuttle. HPCD treatment is used in experiments aiming at the partial depletion of intracellular cholesterol. In order to prevent an increase of intracellular cholesterol through the activation of the mevalonate pathway, cells are also treated with lovastatin while they are fed with a medium containing LDL-free serum. Using a combination of HPCD and lovastatin we find that transcription of the RORE reporter is stimulated in response to cholesterol, epicholesterol and cholestanol and to an even greater extent by cholesterol sulfate and 7-dehydrocholesterol. In contrast all the hydroxycholesterols tested do not display significant activity and the cholesterol derivative 5-cholesten-24β-ethyl-3β-ol-acetate does not trigger any increase in RORα transcriptional activity as compared to vehicle (Table 6). These data correlate well with docking studies on cholesterol derivatives using our X-ray structure of RORα.

Table 6:

Compounds (10μW)	Fold induction	± SEM
Control	1	0.1
Cholesterol	3.3	0.1
Epicholesterol	2.8	0.44
Cholestanol	2.4	0.14
7-Dehydrochol	4.6	0.33
22(R)-OH-Chol	1.2	0.11
25-OH-Chol	1.6	0.06
20(S)-OH-Chol	1.2	0.11
Chol. Sulfate	5.4	0.31
27-OH-Chol	1.5	0.14
5-Cholesten-24beta	1	0.05

Ligand exchange screening by mass spectrometry

(His)₆RORα-LBD269-556 is produced in Sf9 cells and purified by Ni-NTA chromatography followed by size exclusion chromatography. The protein in Tris-HCl buffer at a concentration of 135 μM is incubated overnight at 4 °C, with a 10-fold molar excess of 25-hydroxycholesterol (5-cholesten-3beta, 25-diol) or cholesterol sulfate (5-cholesten-3beta-ol-sulfate). Prior to mass spectrometry analysis, the protein is subjected to fast buffer exchange in 50 mM ammonium acetate pH 7.0 by size exclusion chromatography using disposable Centri°Spin 20 columns (Princeton Separations, Adelphia, NJ) according to manufacturer's instructions. Mass spectrometry is carried out using a Q-Tof (Micromass, Manchester, UK) quadrupole time-of-flight hybrid tandem mass spectrometer equipped with a Micromass Z-type electrospray ionization source (ESI). The acquisition mass range is typically m/z 1500-4500 in 5 seconds. The mass spectrometer is tuned in order to allow detection of multiply-

charged species of non-covalent complexes. The source block temperature and desolvation temperature are kept at 50 °C and 80 °C, respectively. Sample cone voltage (Vc) is set to 23 volts for standard measurements. In-source induced fragmentation experiments are performed by increasing Vc up to 100 volts. The protein solution is infused at a flow rate of 10µL/min. Data are recorded and processed using Masslynx software. Spectra are deconvoluted using MaxEnt analysis software (Micromass, Manchester, UK). The results show that both 25-OH cholesterol and cholesterol sulfate are able to fully displace cholesterol bound to the ROR-LBD. Moreover, the comparison at various cone-voltages (Vc) between the ligand/ROR-LBD-complex and the apo-ROR-LBD (without ligand) indicates that cholesterol and 25-OH cholesterol have a similar stability versus in-source collisions. In contrast, the cholesterol sulfate/ROR-LBD complex is more stable than cholesterol or 25-OH cholesterol complex.

Crystallization and X-ray structure of the complex ROR(alpha)/cholesterol-sulfate at 2.20Å

Resolution: An example of structure based design

All amino acid residues relating to the complex ROR(alpha)/cholesterol-sulfate (e.g. the attached coordinates of the complex with cholesterol-sulfate, Table 9) are numbered according to splice variant Alpha-1 (i.e. P35398-2) of SWISS-PROT entry P35398 (corresponding to the number of a given amino acid according to SWISS-PROT P35398-1 as set out in Figure 1 minus 33). All amino acid residues relating to the complex ROR(alpha)/cholesterol (e.g. the attached coordinates of the complex with cholesterol, Table 8) are numbered according to splice variant Alpha-2 (i.e. P35398-1) of SWISS-PROT entry P35398, except for Figures 7-11, where the numbering used is according to P35398-2, and except in the following discussion of the comparison with the cholesterol-sulfate complex. All amino acid residues specified in the claims are numbered according to splice variant Alpha-2 (i.e. P35398-1) of SWISS-PROT entry P35398, as set out in Figure 1.

The proposal that cholesterol-sulfate is a ligand of ROR(alpha) is a result of structure based design, using the previously determined X-ray structure of ROR(alpha)/cholesterol at 1.63Å resolution. In particular, the latter X-ray structure reveals that in the hydrophilic part of the LBP there is space for a substituent attached to the hydroxy-group of cholesterol, if water molecules are displaced. The presence of three arginines (Arg292, Arg370 and Arg367) and of two free backbone amide nitrogens (NH-Gln289 and NH-Tyr290) strongly suggests a negatively charged substituent with at least two hydrogen-bond acceptor functionalities (e.g. a sulfate-group). Docking studies lead to the prediction that cholesterol-sulfate should have higher affinity than cholesterol. Subsequently it is shown by MS-

- 28 -

analysis that indeed cholesterol bound to ROR(alpha) LBD could be exchanged with cholesterol-sulfate.

The complex ROR(alpha)/cholesterol-sulfate could now be cocrystallized and the X-ray structure of the complex is solved at 2.20Å resolution with an R_{cryst} of 19.4% and R_{free} of 21.9% for data from 20Å to 2.20Å. The observed binding mode shows the following features:

- 1). Cholesterol-sulfate and cholesterol have similar overall modes of binding, but cholesterol-sulfate is displaced slightly (e.g. corresponding C3-atoms by 0.85Å) towards the hydrophilic, positively charged, part of the LBP. This can be explained by the optimization of electrostatic and hydrogen-bond interactions made by the sulfate-group.
- 2.) Seven well-ordered water molecules present for cholesterol in the hydrophilic part of the LBP have been displaced in the complex with cholesterol-sulfate. Only one conserved water molecule is still present which mediates interactions between the sulfate group and NH1-Arg367 and O-Ala330.
- 3.) The sulfate group makes direct hydrogen bond interactions with NH-Gln289, NH-Tyr290 and NH1-Arg370. This confirms the docking hypothesis, which led to the proposal of cholesterol-sulfate.
- 4.) The only significant changes in the protein parts of the complexes of ROR(alpha) with cholesterol and cholesterol-sulfate occur for the sidechain of Ile327 and the loop 1-2 (residues Gln289 and Tyr290).

Molecular Biology, Fermentation, Purification and MS-analysis

Generation of the construct (His) $_6$ ROR α -LBD $_{270-523}$, fermentation and purification are done as described above. The exchange of cholesterol by cholesterol-sulfate is done at 37°C and confirmed by MS-analysis: Cholesterol sulfate is dissolved at 50 mM in DMSO and added at 1.0 mM final concentration to the (His) $_6$ ROR α LBD $_{270-523}$ solution at 73 μ M. The resulting solution is incubated overnight at 37° C and further purified by size exclusion chromatography on a SPX75 column, before concentrating to 17.6 mg/ml for crystallization trials. MS determination of the native complex is done as described previously (Kallen *et al.*, Structure, Vol.10, 1697-1707, 2002). A control experiment is done by incubating the same amount of ROR α LBD protein with 5% DMSO under identical conditions. The protein concentration is approximately 15 μ M in 50mM AcONH4, pH 7.0. Both spectra are recorded under identical conditions with Vc = 20 volts.

Crystallization

The protein used for crystallization is at 17.6 mg/ml, in 100mM NaCl, 50mM Tris-HCl pH7.5, 5mM DTT. An ab inito search for crystallization conditions is undertaken. Trials are performed using a

standard vapor diffusion hanging drop set-up, with VDX crystallization plates and siliconized microscope cover slips from Hampton Research. Crystallization droplets are set up at 4°C by mixing on the coverslips 1.0µl of the protein stock solution with 1.0µl of a crystallization solution.

X-ray Data collection: A single crystal of approximate dimensions 60μm x 60μm x 200μm is mounted with a nylon CryoLoop (Hampton Research) and flash-frozen in a cold nitrogen stream for X-ray data collection at 100K. Diffraction data are collected at the Swiss Light Source (operating at 300mA), beamline X06SA, using a Marresearch CCD detector and an incident monochromatic X-ray beam with 0.9200Å wavelength. In total, 226 images are collected with 1.0° rotation each, using an exposure time of 9sec per frame and a crystal-to-detector distance of 150mm. Raw diffraction data are processed and scaled with the HKL program suite version 1.96.1 (Otwinowski and Minor, 1996). The estimated B-factor by Wilson plot analysis is 32.9 Ų. Crystal data and data collection statistics are shown in Table 7:

Number of crystals	1
Space group	$P2_1$
Unit cell dimensions	a=54.4Å
	b=49.9Å
	c=60.7Å
No. of monomers / a.u.	1
Packing coefficient	3.0ų/Da
Estimated solvent content	58%
Wavelength	0.9200Å
Temperature	100K
Resolution range	20.0 - 2.2Å
No. of observations	57,993
No. of unique reflections	16,541

Overall	
Resolution range	20.0-2.2Å
Data redundancy	3.5
Completeness	99.7%
< Ι/ σ (I)>	16.2
R _{merge} on intensities	0.079

Reflections with $I \ge 3\sigma(I)$	66.4%		
Highest res	olution shell		
Resolution range	2.28-2.20Å		
Data redundancy	2.8		
Completeness	99.4%		
< Ι/ σ (I)>	1.9		
R _{merge} on intensities	0.362		
Reflections with $I \ge 3\sigma(I)$	25.9%		

Structure determination and refinement: The structure is determined using as starting model the coordinates of the complex ROR(alpha)/cholesterol refined to 1.63Å resolution. The program REFMAC version 5.0 (CCP4, Acta Crystallogr. D50, 760-763, 1994) is used for refinement. Bulk solvent correction, an initial anisotropic B factor correction and restrained isotropic atomic B-factor refinement are applied. The refinement target is the maximum-likelihood target using amplitudes. No sigma cut-off is applied on the structure factor amplitudes. Cross-validation is used throughout refinement using a test set comprising 5.0% (829) of the unique reflections. Water molecules are identified with the program ARP/wARP and selected based on difference peak height (greater than 3.0°c) and distance criteria. Water molecules with temperature factors greater than 70Ų are rejected. The program O version 7.0 (A.Jones et al., 1991) is used for model rebuilding. The refinement statistics for the final model are shown in Table 2. The final model of the complex ROR(alpha)/cholesterol-sulfate has good geometry (rms bond lengths = 0.014Å, rms bond angles = 1.41°) and no residues are in a disallowed region of the Ramachandran plot.

Crystallization, data collection: The crystals used for data collection are obtained with a well solution composed of 0.2M MgCl₂, 16% w/v PEG4000, 0.1M Tris HCl, pH 8.5. The crystals reached maximal dimensions of up to 0.2 mm within 6 weeks. The complex of ROR α LBD with cholesterol-sulfate is thus crystallized in a crystal form with a=54.4Å, b=49.9Å, c=60.7Å, β =97.8°, P2₁ and 1 complex/asymmetric unit, which is similar to the crystal form previously obtained in the complex with cholesterol.

Conformation of cholesterol-sulfate bound to ROR(alpha) and its interactions: In general, the electron density is of excellent quality, except for amino acids 461-464 (L9-10), which has only weak density. The protein part of the refined model consists of the last two His-amino acids from the His-tag,

- 31 -

followed by the PreScissionTM-site (LEVLFQG) and by amino acids 271-511 of the RORα-LBD. The refined model also contains 256 water molecules and 1 cholesterol-sulfate molecule. The sulfate group makes direct hydrogen bond interactions with NH-Gln289 (3.0Å), NH-Tyr290 (2.9Å) and a bidentate interaction with NH1-Arg370 (3.0Å, 3.1Å). A water-mediated interaction is made with NH1-Arg367.

Comparison of the X-ray structures of cholesterol-sulfate and cholesterol bound to ROR(alpha) LBD Figure 10 shows a superposition (using Ca's of the respective LBD's) for the ROR(alpha) complexes with cholesterol and cholesterol-sulfate. The r.m.s.d for the Cα atoms of residues Pro270-Phe511 after superposition is 0.26Å. The only significant changes in the protein parts occur for the sidechain of Ile327 and the loop 1-2 (residues Gln289 and Tyr290): The backbone NH-atoms for Gln289 and Tyr290 move by ca. 0.8Å towards the sulfate-group (with a concomitant movement of the respective sidechains), in order to improve the interactions with the sulfate-group. The sidechain of Ile327 has to move slightly, in order to avoid a steric clash with the terminal isopropyl-group (Figure .9). The comparison shows that cholesterol-sulfate and cholesterol have similar overall modes of binding, but cholesterol-sulfate is displaced slightly (e.g. corresponding C3-atoms by 0.85Å and corresponding C2-atoms by 0.7Å) towards the hydrophilic, positively charged, part of the LBP (Figure 9). This can be explained by the optimization of electrostatic and hydrogen-bond interactions made by the sulfategroup. 7 well-ordered water molecules present for cholesterol in the hydrophilic part of the LBP have been displaced in the complex with cholesterol-sulfate (Figure 10). Only one conserved water molecule is still present which mediates interactions between the sulfate group and NH1-Arg367 and O-Ala330. The sulfate group makes direct hydrogen bond interactions with NH-Gln289, NH-Tyr290 and NH1-Arg370. This confirms the docking hypothesis, which led to the proposal of cholesterolsulfate.

TABLE 8

TAULUS	J								
ATOM		1	CB	HIS A	308	-3.470	26.612	-1.587	1.00 57.47
ATOM		2	CG	HIS A		-4.960	26.750	-1.571	1.00 68.25
ATOM		3		HIS A		-5.766	27.800	-1.862	1.00 72.02
ATOM		4		HIS A		-5.794	25.720	-1.190	1.00 71.55
		5		HIS A		-7.049	26.131	-1.245	1.00 75.57
ATOM		6		HIS A		-7.061	27.389	-1.652	1.00 73.93
MOTA						-1.527	26.518	-0.048	1.00 46.68
ATOM		7	C	HIS A		-1.408	25.970	1.039	1.00 46.34
ATOM		8	0			-2.472	28.682	-0.665	1.00 46.21
ATOM		9	N	HIS A		-2.472	27.256	-0.390	1.00 50.95
ATOM		10	CA	HIS A		-0.598	26.489	-0.995	1.00 43.13
ATOM		11	N	LEU A			25.856	-0.780	1.00 43.49
MOTA		12	CA	LEU A		0.692 1.517	25.900	-2.069	1.00 41.03
ATOM		13	CB	LEU A			25.402	-2.009	1.00 39.69
ATOM		14	CG	LEU A		2.967	23.898	-1.765	1.00 39.26
ATOM		15		LEU A		2.988	25.742	-3.348	1.00 33.46
MOTA		16		LEU A		3.668	26.673	0.307	1.00 33.40
MOTA		17	C	LEU A		1.397	26.121	1.217	1.00 39.43
MOTA		18	0	LEU A		1.987	27.994	0.158	1.00 41.63
ATOM		19	N	ALA A		1.371	28.894	1.125	1.00 43.60
ATOM		20	CA	ALA A		$1.972 \\ 1.772$	30.334	0.692	1.00 41.23
MOTA		21	CB	ALA A		1.772	28.638	2.494	1.00 44.99
ATOM		22	C	ALA A	310		28.454	3.487	1.00 42.70
ATOM		23	0	ALA A	310	2.028		2.531	1.00 46.22
ATOM		24	N	GLN A		-0.011	28.589	3.767	1.00 48.70
MOTA		25	CA	GLN A		-0.765	28.330		1.00 48.70
ATOM		26	CB	GLN A		-2.266	28.239	3.472	1.00 53.01
ATOM		27	CG	GLN A		-3.081	29.513	3.686	1.00 09.31
ATOM		28	CD	GLN A		-4.596	29.289	3.479	1.00 78.89
ATOM		29	OE1			-5.137	28.224	3.832	1.00 83.81
MOTA		30	NE2			-5.275	30.278	2.876	1.00 82.00
MOTA		31	C	GLN A		-0.339	27.015	4.413	1.00 43.78
MOTA		32	0	GLN A		-0.043	26.949	5.599	1.00 43.47
MOTA		33	M	ASN A		-0.332	25.966	3.604	1.00 43.06
MOTA		34	CA	ASN A		0.023	24.624	4.049	1.00 43.00
MOTA		35	CB	ASN A		-0.236	23.632	2.918	1.00 52.50
MOTA		36	CG	ASN A		0.867	22.607	2.776 3.173	1.00 04.44
ATOM		37	OD1			0.709	21.453	2.191	1.00 70.50
MOTA		38	ND2			1.992 1.437	23.017 24.436	4.606	1.00 40.68
ATOM		39	C	ASN A		1.635	23.638	5.518	1.00 39.27
ATOM		40	0	ASN A		2.424	25.072	3.974	1.00 39.40
ATOM		41	N	ILE A		3.824	24.979	4.407	1.00 38.82
ATOM		42	CA	ILE A		4.802	25.421	3.253	1.00 34.58
ATOM		43	CB	ILE A		6.169	25.806	3.799	1.00 36.01
ATOM		44	CG2	ILE A		4.956	24.284	2.240	1.00 37.16
ATOM		45		ILE A		6.005	24.537	1.154	1.00 35.61
MOTA		46			212	4.030		5.703	1.00 37.29
ATOM		47	C	ILE A	313	4.786	25.399	6.585	1.00 39.16
MOTA		48	O N	SER A		3.298	26.906	5.823	1.00 35.32
MOTA		49	N	SER A	311	3.334	27.790	6.989	1.00 36.43
MOTA		50 51	CA	SER A		2.457	29.014	6.728	1.00 37.35
MOTA		51 52	CB	SER A		3.059	29.848	5.759	1.00 41.24
ATOM		52 53	OG C	SER A		2.807	27.089	8.241	1.00 35.85
ATOM		53 54	C	SER A		3.305	27.283	9.351	1.00 36.16
ATOM		54 55	O M	LYS A		1.777	26.288	8.033	1.00 35.61
ATOM		56	N CA	LYS A	315	1.131	25.547	9.094	1.00 36.35
ATOM ATOM		57	CB	LYS A		-0.183	24.969	8.564	1.00 34.96
ATOM		58	CG	LYS A	315	-1.051	24.316	9.597	1.00 38.82
ATOM		59	CD	LYS A	315	-2.470	24.232	9.084	1.00 49.73
ATOM		60	CE	LYS A	315	-3.386	23.556	10.082	1.00 56.14
ATOM		61	NZ	LYS A	315	-3.021	22.113	10.247	1.00 65.23
ATOM		62	C	LYS A	315	2.056	24.438	9.571	1.00 36.74
MOTA		63	ŏ	LYS A		2.102	24.130	10.757	1.00 38.14
HI OH		55	_						

WO 03/093312

ATOM	64	N	SER A	316	2.771	23.835	8.624	1.00	35.23
ATOM	65	ĈA	SER A		3.708	22.757	8.904	1.00	31.03
		CB	SER A		4.268	22.189	7.591		33.89
ATOM	66				3.275	21.504	6.838		36.00
MOTA	67	OG.	SER A				9.769		31.80
MOTA	68	С	SER A		4.842	23.293			
MOTA	69	0	SER A		5.223	22.667	10.760		30.02
ATOM	70	N	HIS A	317	5.391	24.440	9.354	1.00	29.40
ATOM	71	CA	HIS A		6.468	25.128	10.078	1.00	31.38
ATOM	72	CB	HIS A		6.838	26.397	9.319	1.00	28.86
			HIS A		7.765	27.317	10.058	1.00	30.88
ATOM	73	CG			7.590	28.583	10.506	1.00	31.39
ATOM	74	CD2	HIS A	31/				1.00	31.14
MOTA	75		HIS A	317	9.085	27.007	10.310		
MOTA	76	CE1	HIS A		9.686	28.042	10.866	1.00	
ATOM	77	NE2	HIS A	317	8.801	29.012	10.996	1.00	30.99
ATOM	78	С	HIS A	317	5.964	25.489	11.486	1.00	32.96
ATOM	79	Ö	HIS A	317	6.647	25.271	12.491	1.00	30.21
	80	Ň	LEU A		4.766	26.066	11.519	1.00	35.80
MOTA		CA	LEU A		4.099	26.456	12.754	1.00	39.30
ATOM	81				2.651	26.888	12.454	1.00	42.10
ATOM	82	CB	LEU A				13.629	1.00	45.53
MOTA	83	CG	LEU A		1.664	27.026			
MOTA	84	CD1	LEU A		1.898	28.331	14.354	1.00	42.84
MOTA	85	CD2	LEU A	318	0.233	26.963	13.127		46.58
ATOM	86	С	LEU A	318	4.070	25.267	13.708	1.00	39.53
ATOM	87	0	LEU A		4.581	25.337	14.829	1.00	45.11
ATOM	88	N	GLU A		3.517	24.157	13.235	1.00	34.75
	89	CA	GLU A		3.378	22.951	14.040	1.00	31.78
ATOM					2.258	22.088	13.464	1.00	35.64
ATOM	90	CB	GLU A				13.304	1.00	
MOTA	91	CG	GLU A		0.966	22.887			
ATOM	92	CD	GLU A		-0.204	22.079	12.797		48.29
MOTA	93	OE1	GLU A	319	-0.046	20.870	12.496	1.00	51.24
MOTA	94	OE2	GLU A	319	-1.299	22.675	12.715		49.93
ATOM	95	С	GLU A	319	4.605	22.092	14.335	1.00	31.28
ATOM	96	Ō	GLU A		4.501	21.150	15.128	1.00	29.74
ATOM	97	N	THR A		5.749	22.374	13.703	1.00	29.30
	98	CA	THR A		6.948	21.589	13.957	1.00	25.31
MOTA	-		THR A		7.428	20.826	12.723	1.00	26.81
ATOM	99	CB				21.760	11.697	1.00	31.74
ATOM	100	OG1	THR A		7.760			1.00	25.26
MOTA	101	CG2			6.371	19.874	12.228		
MOTA	102	С	THR A		8.086	22.435	14.499	1.00	27.08
MOTA	103	0	THR A	320	9.251	22.078	14.369	1.00	28.40
MOTA	104	N	CYS A	321	7.754	23.591	15.058	1.00	27.84
ATOM	105	CA	CYS A		8.758	24.440	15.690	1.00	32.58
ATOM	106	CB		321	8.575	25.897	15.291	1.00	35.52
ATOM	107	SG	CYS A		9.587	26.379	13.907	1.00	31.41
	108	c	CYS A		8.481	24.273	17.183	1.00	33.42
ATOM			CYS A		7.315	24.272	17.584	1.00	33.09
MOTA	109	0			9.516	24.122	18.005		33.42
ATOM	110	N	GLN A						
MOTA	111	CA	GLN A		9.280	23.945	19.435		37.77
MOTA	112	CB	GLN A		10.566	23.575	20.159		38.95
ATOM	113	CG	GLN A	322	10.311	23.332	21.638		41.00
ATOM	114	CD	GLN A	322	11.474	22.709	22.355		43.45
ATOM	115	OE1			12.639	22.892	21.974	1.00	45.86
ATOM	116	NE2			11.173	21.973	23.408	1.00	43.47
	117	C	GLN A	322	8.595	25.133	20.143	1.00	38.21
MOTA			CIN A	222		24.945	20.891		40.89
MOTA	118	0	GLN A		7.627				37.01
MOTA	119	N	TYR A	323	9.087	26.348	19.893		
MOTA	120	CA	TYR A	323	8.518	27.545	20.513	1.00	39.53
ATOM	121	CB	TYR A		9.576	28.318	21.306		37.75
MOTA	122	CG	TYR A	323	10.245	27.509	22.370		36.25
MOTA	123		TYR A		11.551	27.058	22.191		40.18
ATOM	124	CE1	TYR A	323	12.185	26.279	23.139	1.00	43.63
ATOM	125	CD2		323	9.576	27.164	23.537		38.29
	126	CE2			10.196	26.386	24.500		43.87
ATOM			TYR A		11.508	25.945	24.294		45.72
ATOM	127	CZ	TIK A	222	12.165	25.182	25.236		50.91
ATOM	128	ОН	TYR A						41.39
MOTA	129	С	TYR A	343	7.916	28.496	19.502	1.00	41.33

	120	^	TYR A 32	2	8.185	28.404	18.302	1.00	43.21
MOTA	130	0				29.451	20.011		38.45
MOTA	131	N	LEU A 32		7.149				
ATOM	132	CA	LEU A 32	4	6.556	30.442	19.158		36.36
MOTA	133	CB	LEU A 32	4	5.260	30.960	19.761		40.65
ATOM	134	ĊĠ	LEU A 32		4.135	29.917	19.804	1.00	47.37
					3.021	30.333	20.790		48.02
ATOM	135	CD1							48.49
MOTA	136	CD2	LEU A 32		3.569	29.698	18.390		
ATOM	137	С	LEU A 32	4	7.586	31.548	19.037		36.82
MOTA	138	0	LEU A 32	4	8.369	31.791	19.955	1.00	35.71
ATOM	139	N	ARG A 32		7.604	32.185	17.876	1.00	33.86
			ARG A 32	Ĕ	8.519	33.274	17.595	1.00	34.00
ATOM	140	CA	ARG A 32	_			16.252		32.60
ATOM	141	CB	ARG A 32	2	8.132	33.913			29.17
MOTA	142	CG	ARG A 32		9.087	34.947	15.744		
MOTA	143	CD	ARG A 32	5	10.477	34.371	15.667		30.77
ATOM	144	NE	ARG A 32	5	11.388	35.268	14.984	1.00	31.48
	145	CZ	ARG A 32		11.340	35.518	13.681	1.00	41.33
MOTA			ARG A 32	5	10.421	34.931	12.912		39.89
MOTA	146	NH1							42.61
MOTA	147	NH2	ARG A 32		12.195	36.383	13.147		
ATOM	148	С	ARG A 32	5	8.462	34.328	18.711		36.35
ATOM	149	0	ARG A 32	5	9.503	34.826	19.145	1.00	37.18
ATOM	150	N	GLU A 32		7.244	34.639	19.169	1.00	39.65
			GLU A 32		6.985	35.626	20.226	1.00	41.32
MOTA	151	CA				35.784	20.459		46.07
MOTA	152	CB	GLU A 32		5.487		19.272		65.71
ATOM	153	CG	GLU A 32		4.720	36.379			
ATOM	154	CD	GLU A 32	6	4.555	35.424	18.062		72.41
ATOM	155	OE1	GLU A 32	6	4.261	34.214	18.267		74.04
ATOM	156	OE2	GLU A 32	6	4.696	35.904	16.901	1.00	73.55
	157	C	GLU A 32		7.659	35.211	21.520	1.00	38.16
ATOM			GLU A 32		8.332	36.023	22.148	1.00	35.77
MOTA	158	0			7.487	33.938	21.880		35.48
ATOM	159	N	GLU A 32						38.23
ATOM	160	CA	GLU A 32		8.092	33.353	23.077		
ATOM	161	CB	GLU A 32	7	7.911	31.833	23.082		46.45
ATOM	162	CG	GLU A 32	7	6.486	31.293	23.134		57.52
ATOM	163	CD	GLU A 32	7	6.452	29.752	23.125	1.00	63.49
ATOM	164	OE1			7.441	29.113	23.557	1.00	68.14
	165	OE2			5.445	29.172	22.667	1.00	68.00
MOTA			GLU A 32		9.599	33.615	23.140	1 00	34.14
ATOM	166	C	GLU A 32	<u>'</u>		34.218	24.076		34.19
ATOM	167	0	GLU A 32		10.098				
ATOM	168	N	LEU A 32		10.304	33.158	22.114		29.72
MOTA	169	CA	LEU A 32	8	11.748	33.293	22.006		29.32
ATOM	170	CB	LEU A 32	8	12.217	32.636	20.712		29.59
ATOM	171	CG	LEU A 32		12.016	31.131	20.626	1.00	30.01
ATOM	172		LEU A 32		11.986	30.725	19.164	1.00	31.46
			LEU A 32		13.119	30.432	21.367	1.00	22.42
MOTA	173				12.267	34.715	22.041		28.85
MOTA	174	C	LEU A 32						29.43
ATOM	175	0	LEU A 32		13.366	34.954	22.518		
ATOM	176	N	GLN A 32	9	11.486	35.654	21.520		33.80
MOTA	177	CA	GLN A 32	9	11.901		21.481		37.54
MOTA	178	CB	GLN A 32	:9	11.093	37.808	20.439	1.00	43.64
ATOM	179	CG	GLN A 32		11.132	37.198	19.050	1.00	53.22
ATOM	180	CD	GLN A 32		10.283	37.983	18.065		59.04
			CINI A 32		9.035	37.966	18.127		59.51
ATOM	181		GLN A 32	9			17.174		59.14
ATOM	182	NE2			10.953	38.720		1.00	35.96
ATOM	183	С	GLN A 32		11.725	37.721	22.846		
MOTA	184	0	GLN A 32	.9	12.525	38.562	23.241		30.61
ATOM	185	N	GLN A 33	0	10.695	37.308	23.572		36.62
ATOM	186	CA	GLN A 33		10.450	37.846	24.901		41.09
ATOM	187	CB	GLN A 33	0	9.093	37.383	25.391		45.78
			GLN A 33	i n	7.957	37.930	24.579		63.61
MOTA	188	CG	OLYL W DO	. 0		37.133	24.784		74.77
ATOM	189	CD	GLN A 33		6.686				79.50
MOTA	190		GLN A 3	U	6.569	36.365	25.750		
MOTA	191	NE2			5.730	37.285	23.865		82.47
ATOM	192	C	GLN A 33		11.515	37.477	25.951		38.55
ATOM	193	0	GLN A 33		11.609	38.135	26.979		41.30
ATOM	194	N	ILE A 33	1	12.305	36.429	25.715		32.00
MOTA	195	CA	ILE A 3		13.313	36.015	26.686	1.00	23.76
111 011				_		_			

ATOM	196	СВ	ILE A	331	13.078	34.596	27.169	1.00	22.66
	197	CG2	ILE A		11.656	34.435	27.630	1.00	21.34
MOTA		CG1	ILE A	331	13.355	33.619	26.053	1.00	24.33
MOTA	198				13.364	32.235	26.555	1.00	23.84
MOTA	199	CD1	ILE A			36.183	26.205		23.46
ATOM	200	С	ILE A	331	14.738				27.34
ATOM	201	0	ILE A	331	15.657	35.455	26.592		
ATOM	202	N	THR A	332	14.918	37.180	25.354		23.06
ATOM	203	CA	THR A	332	16.204	37.521	24.799		23.34
ATOM	204	CB	THR A	332	15.962	38.552	23.680	1.00	31.64
	205	OG1			16.261	37.954	22.404	1.00	35.81
ATOM			THR A	333	16.735	39.863	23.912	1.00	37.99
ATOM	206	CG2	THR A		17.180	38.051	25.857		20.21
MOTA	207	C				37.887	25.749		21.02
MOTA	208	0	THR A		18.401				25.18
MOTA	209	N	TRP A		16.628	38.683	26.886		
ATOM	210	CA	TRP A		17.437	39.226	27.988		23.07
ATOM	211	CB	TRP A	333	16.582	40.108	28.879		19.83
MOTA	212	CG	TRP A		15.407	39.426	29.504		17.19
MOTA	213	CD2	TRP A		15.344	38.851	30.820	1.00	22.36
	214	CE2	TRP A		14.030	38.392	31.008	1.00	26.11
MOTA			TRP A		16.274	38.693	31.865	1.00	22.59
MOTA	215	CE3			14.172	39.294	28.974	1.00	14.35
MOTA	216	CD1	TRP A			38.671	29.858		19.63
ATOM	217	NE1	TRP A	333	13.336		32.213		25.43
MOTA	218	CZ2	TRP A		13.607	37.778	32.213		21.23
MOTA	219	CZ3	TRP A		15.852	38.082	33.056		
ATOM	220	CH2	TRP A	333	14.538	37.636	33.216		20.18
ATOM	221	С	TRP A	333	18.028	38.116	28.826		23.38
ATOM	222	Ō	TRP A	333	19.030	38.314	29.500		27.96
ATOM	223	N	GLN A		17.436	36.925	28.730	1.00	24.06
	224	CA	GLN A		17.893	35.767	29.492	1.00	22.85
ATOM			GLN A		16.804	34.712	29.586	1.00	22.07
ATOM	225	CB			15.575	35.251	30.240		25.58
MOTA	226	CG	GLN A			34.228	30.427		29.55
MOTA	227	CD	GLN A		14.492				32.54
MOTA	228	OE1			14.621	33.066	30.029		
MOTA	229	NE2	GLN A	334	13.388	34.664	31.006		31.52
ATOM	230	С	GLN A	334	19.169	35.145	29.016	1.00	
ATOM	231	0	GLN A	334	19.180	34.020	28.519		27.49
ATOM	232	N	THR A		20.257	35.878	29.179	1.00	21.73
ATOM	233	CA.	THR A	335	21.566	35.403	28.804	1.00	20.96
	234	CB	THR A	335	22.436	36.595	28.396	1.00	26.82
MOTA		OG1		335	22.471	37.528	29.487	1.00	25.70
ATOM	235				21.881	37.286	27.109	1.00	
ATOM	236	CG2			22.237	34.647	29.978	1.00	
ATOM	237	C	THR A		22.237	34.762	31.133		25.14
ATOM	238	0	THR A				29.682	1.00	
ATOM	239	N	PHE A		23.306	33.902			27.78
ATOM	240	ca	PHE A		24.048	33.138	30.693		
ATOM	241	CB	PHE A		25.036	32.126	30.051		23.18
ATOM	242	CG	PHE A	336	24.385	30.861	29.569		24.30
ATOM	243	CD1	PHE A	336	24.236	30.615	28.193		24.39
ATOM	244	CD2		336	23.855	29.952	30.477		18.74
ATOM	245		PHE A		23.558	29.484	27.734		19.18
	245	CE2		336	23.174	28.824	30.043		20.30
ATOM			PHE A		23.018	28.582	28.667		24.72
ATOM	247	CZ	PRE A	226	24.835	34.058	31.632		30.11
MOTA	248	C	PHE A					1 00	27.94
MOTA	249	0	PHE A	336	25.560	34.953	31.182		
MOTA	250	N	LEU A	337	24.682	33.840	32.934		29.31 30.51
ATOM	251	CA	LEU A	337	25.413	34.631	33.921		
ATOM	252	CB	LEU A		24.920	34.293	35.339		30.83
ATOM	253	CG	LEU A	337	23.426	34.451	35.652		27.00
ATOM	254		LEU A	337	23.096	33.895	37.023		28.96
ATOM	255	CD2	LEU A	337	23.047	35.915	35.568		29.51
MOTA	256	C	LEU A	337	26.902	34.311	33.755	1.00	30.04
	257	Ö	LEU A		27.247	33.289	33.180	1.00	31.12
MOTA			GLN A		27.779	35.200	34.226		32.35
ATOM	258	N	GLN A		29.231	35.036	34.098		32.95
ATOM	259	CA			29.231	36.189	34.782		36.81
MOTA	260	CB	GLN A	220			34.702		45.74
MOTA	261	CG	GLN A	330	31.330	36.423	74.614	4.00	43.74

ATOM	262	CD GLN A 338	31.29	2 36.625	32.691	1.00 60.39
	263	OE1 GLN A 338	_		32.158	1.00 62.23
MOTA					31.985	1.00 63.44
MOTA	264	NE2 GLN A 338	-		34.616	1.00 32.21
ATOM	265	C GLN A 338				
ATOM	266	O GLN A 338			34.122	
ATOM	267	N GLU A 339	29.21	2 33.234	35.681	1.00 33.70
	268	CA GLU A 339		5 31.989	36.297	1.00 35.07
ATOM					37.611	1.00 42.66
ATOM	269	CB GLU A 339			38.449	1.00 55.90
ATOM	270	CG GLU A 33			38.127	1.00 58.95
ATOM	271	CD GLU A 339				1.00 47.67
ATOM	272	OE1 GLU A 339		3 34.992	38.255	
ATOM	273	OE2 GLU A 339	26.32	5 33.023	37.771	1.00 67.60
ATOM	274	C GLU A 33	29.34	0 30.878	35.319	1.00 27.81
ATOM	275	O GLU A 33	30.15		35.062	1.00 26.00
		N GLU A 34			34.795	1.00 26.98
ATOM	276				33.831	1.00 28.10
ATOM	277	CA GLU A 34			33.457	1.00 29.51
MOTA	278	CB GLU A 34			34.636	1.00 26.99
ATOM	279	CG GLU A 34		30.053		1.00 30.46
ATOM	280	CD GLU A 34			34.284	
MOTA	281	OE1 GLU A 34			34.510	1.00 34.56
ATOM	282	OE2 GLU A 34	23.58	30 31.471	33.802	1.00 31.24
	283	C GLU A 34		73 29.875	32.592	1.00 25.22
ATOM		O GLU A 34			32.096	1.00 24.52
ATOM	284				32.126	1.00 23.36
ATOM	285				30.953	1.00 28.31
MOTA	286	CA ILE A 34			30.391	1.00 27.91
MOTA	287	CB ILE A 34			20.321	1.00 23.19
ATOM	288	CG2 ILE A 34			29.382	
ATOM	289	CG1 ILE A 34	1 28.79	33.040	29.718	1.00 26.01
ATOM	290	CD1 ILE A 34	1 28.7	72 34.533	29.426	1.00 26.73
ATOM	291	C ILE A 34	1 31.23	10 30.382	31.208	1.00 29.36
	292	O ILE A 34			30.388	1.00 29.02
ATOM					32.372	1.00 36.68
MOTA	293				32.700	1.00 37.76
MOTA	294	CA GLU A 34			34.011	1.00 50.01
ATOM	295	CB GLU A 34				1.00 68.37
ATOM	296	CG GLU A 34	2 32.8		35.298	
MOTA	297	CD GLU A 34	2 32.9		36.006	1.00 77.44
ATOM	298	OE1 GLU A 34	2 34.1		36.384	1.00 81.72
ATOM	299	OE2 GLU A 34	2 31.9	38 28.398	36.218	1.00 79.74
ATOM	300	C GLU A 34		69 28.567	32.793	1.00 29.07
	301	O GLU A 34			32.421	1.00 25.34
ATOM					33.316	1.00 28.65
ATOM	302	N ASN A 34			33.459	1.00 31.12
ATOM	303	CA ASN A 34			34.113	1.00 31.12
MOTA	304	CB ASN A 34			34.268	1.00 44.07
MOTA	305	CG ASN A 34				1.00 52.87
ATOM	306	OD1 ASN A 34			34.857	
ATOM	307	ND2 ASN A 34			33.658	1.00 49.75
ATOM	308	C ASN A 34	3 31.6	93 26.050	32.091	1.00 31.48
ATOM	309	O ASN A 34		74 25.106	31.939	1.00 32.73
ATOM	310	N TYR A 34			31.089	1.00 31.34
					29.720	1.00 27.38
MOTA	311	CA TYR A 34			28.747	1.00 19.95
ATOM	312	CB TYR A 34				1.00 15.00
MOTA	313	CG TYR A 34				1.00 13.00
MOTA	314	CD1 TYR A 34	4 27.8		29.313	1.00 12.78
ATOM	315	CE1 TYR A 34	4 26.4		29.464	
ATOM	316	CD2 TYR A 34	4 28.1		28.649	1.00 16.37
ATOM	317	CE2 TYR A 34	4 26.8	05 24.939	28.802	1.00 17.65
ATOM	318	CZ TYR A 34			29.210	1.00 14.48
	319	OH TYR A 34				1.00 15.05
ATOM						1.00 27.55
ATOM	320	C TYR A 34				1.00 30.70
MOTA	321	O TYR A 34	14. J4. J			1.00 28.25
MOTA	322	N GLN A 34	33.1			1.00 20.23
MOTA	323	CA GLN A 34			20.340	
MOTA	324	CB GLN A 34	34.9			1.00 29.90
ATOM	325	CG GLN A 34	15 34.2			1.00 35.96
MOTA	326	CD GLN A 34	l5 34.8			1.00 40.32
MOTA	327	OE1 GLN A 34	15 35.6	54 31.469	29.187	1.00 43.48
232 021	55,					

MOTA	328	NE2	GLN A	345	34.375	32.101	27.469	1.00	40.57
ATOM	329	C	GLN A		35.397	26.446	29.668	1.00	36.16
ATOM	330	ŏ	GLN A		36.485	26.128	29.179		36.49
ATOM	331	N	ASN A		34.972	26.004	30.853		42.02
ATOM	332	CA	ASN A		35.780	25.077	31.630		42.72
MOTA	333	CB	ASN A	346	35.532	25.237	33.135		48.26
ATOM	334	CG	ASN A	346	36.336	26.398	33.743		52.40
ATOM	335	OD1	ASN A	346	37.433	26.728	33.282		53.04
MOTA	336		ASN A		35.802	26.995	34.799		53.36
MOTA	337	С	ASN A		35.633	23.619	31.189		40.45
MOTA	338	0	ASN A		36.533	22.810	31.475		38.19
ATOM	339	N	LYS A		34.559	23.293	30.449		32.64
MOTA	340	CA	LYS A		34.351	21.912	29.980 29.338	1 00	26.11 22.43
MOTA	341	CB	LYS A		32.985	21.742 22.141	30.218		21.17
MOTA	342	CG	LYS A		31.860 30.533	21.903	29.569		25.53
ATOM	343	CD	LYS A		29.436	22.235	30.550		31.64
ATOM	344	CE	LYS A LYS A		28.105	21.911	30.002		42.98
MOTA	345 346	NZ C	LYS A		35.417	21.514	28.979		25.51
MOTA	347	Ö	LYS A		35.862	22.338	28.186		30.14
ATOM ATOM	348	N	GLN A		35.873	20.269	29.058		23.11
ATOM	349	CA	GLN A		36.891	19.771	28.128	1.00	29.12
ATOM	350	CB	GLN A		37.252	18.338	28.502		37.39
ATOM	351	CG	GLN A		37.330	18.100	30.007	1.00	50.83
ATOM	352	CD	GLN A		38.742	17.956	30.494	1.00	55.85
ATOM	353	OE1	GLN A	348	39.428	17.011	30.122	1.00	
ATOM	354	NE2	GLN A	348	39.190	18.883	31.342	1.00	
ATOM	355	С	GLN A	348	36.292	19.803	26.704		25.62
ATOM	356	0	GLN A		35.067	19.729	26.570		25.40
ATOM	357	N	ARG A		37.137	19.854	25.668		28.86
MOTA	358	CA	ARG A		36.671	19.928	24.271	1.00	30.13
MOTA	359	CB	ARG A		37.831	19.768	23.276		38.59 51.14
MOTA	360	CG	ARG A		37.408	20.068 19.932	21.821 20.772		60.22
ATOM	361	CD	ARG A		38.539 38.121	20.510	19.481		71.23
ATOM	362	NE	ARG A ARG A		38.525	20.126	18.263	1.00	
ATOM	363	CZ	_		39.392	19.130	18.090		72.73
ATOM	364 365	NH1 NH2			38.041	20.753	17.198	1.00	
ATOM ATOM	366	C	ARG A		35.578	18.940	23.908	1.00	
MOTA	367	ŏ	ARG A		34.527	19.322	23.387	1.00	26.63
ATOM	368	Ŋ	GLU A		35.857	17.662	24.165		29.38
ATOM	369	CA	GLU A		34.932	16.565	23.877		27.83
ATOM	370	CB	GLU A	350	35.586	15.215	24.184	1.00	
ATOM	371	CG	GLU A	350	35.794	14.956	25.684		35.99
ATOM	372	$^{\mathtt{CD}}$	GLU A		37.212	15.247	26.148		38.01
MOTA	373	OE1			37.736	14.408	26.913		43.71
MOTA	374		GLU A	350	37.809	16.283	25.756		32.70 24.52
ATOM	375	C	GLU A	350	33.640	16.687	24.654 24.195		25.09
MOTA	376	0	GLU A	350	32.596	16.237 17.268	25.847		22.09
ATOM	377	N	VAL A		33.709 32.513	17.457	26.645		20.23
ATOM	378	CA	VAL A VAL A		32.854	17.885	28.107		20.75
ATOM	379	CB CC1	VAL A VAL A		31.583	18.062	28.911		19.11
ATOM	380 381	CG2			33.778	16.851	28.759		24.36
ATOM	382	C	VAL A		31.625	18.521	25.990		20.47
ATOM ATOM	383	ŏ	VAL A		30.405	18.343	25.878		21.64
ATOM	384	N	MET A		32.211	19.646	25.592	1.00	23.84
ATOM	385	CA	MET A	352	31.414	20.705	24.952		23.93
ATOM	386	CB	MET A		32.235	22.008	24.824		28.98
ATOM	387	CG	MET A		31.437	23.318	24.552		26.03
ATOM	388	SD	MET A	352	30.054	23.586	25.661		27.59
ATOM	389	CE	MET A	352	29.087	24.826	24.802		28.37
ATOM	390	C	MET A		30.897	20.191	23.580		21.58
MOTA	391	0	MET A		29.743	20.392	23.241		23.25
MOTA	392	N	TRP A		31.714	19.450	22.847		20.93
ATOM	393	CA	TRP A	353	31.249	18.904	21.567	T.00	22.11

MOTA MOTA MOTA MOTA MOTA MOTA MOTA MOTA	394 395 396 397 398 399 400 401 402	CG CD2 CE2 CE3 CD1 CE2 CZ2 CZ3 C	TRP A 353	32.375 33.205 33.052 34.093 32.135 34.298 34.838 34.248 32.291	18.137 18.935 18.969 19.776 18.385 19.711 20.216 20.015 18.623	20.884 19.922 18.489 17.974 17.592 20.209 19.038 16.599 16.228 15.748	1.00 1.00 1.00 1.00 1.00 1.00 1.00	23.30 29.85 29.97 30.39 30.52 30.84 32.97 32.23 29.92 30.15
MOTA MOTA	403 404		TRP A 353 TRP A 353	33.344 30.022	19.432 17.992	21.733	1.00	19.54
MOTA	405	-	TRP A 353 GLN A 354	29.027 30.059	18.132 17.088	21.014 22.714		21.17 20.89
MOTA MOTA	406 407		GLN A 354 GLN A 354	28.938	16.158	22.939	1.00	19.30
MOTA	408	CB	GLN A 354	29.263	15.167	24.077 24.093	1.00	23.50 24.75
ATOM ATOM	409 410		GLN A 354 GLN A 354	28.393 27.436	13.888 13.788	25.282		23.74
ATOM	411	OE1	GLN A 354	27.297	14.737	26.049		29.52
MOTA	412		GLN A 354	26.767 27.647	12.629 16.875	25.427 23.248		20.53
ATOM ATOM	413 414		GLN A 354 GLN A 354	26.566	16.516	22.759	1.00	16.41
MOTA	415	N	LEU A 355	27.747	17.885	24.098		19.29 15.90
MOTA	416 417		LEU A 355 LEU A 355	26.574 26.913	18.645 19.657	24.468 25.579		15.22
ATOM ATOM	418	CG	LEU A 355	25.802	20.622	25.993	1.00	17.93
MOTA	419	CD1	LEU A 355	24.582 26.418	19.962 21.667	26.610 26.918		14.68 21.31
ATOM ATOM	420 421		LEU A 355 LEU A 355	25.993	19.357	23.240		11.91
ATOM	422	Ō	LEU A 355	24.790	19.348	23.054		14.23
MOTA	423		CYS A 356	26.827 26.307	20.005 20.691	22.441 21.244		16.77 22.19
MOTA MOTA	424 425		CYS A 356 CYS A 356	27.436	21.450	20.561	1.00	21.05
MOTA	426	SG	CYS A 356	28.067	22.797	21.523		23.18 21.08
ATOM	427 428	0	CYS A 356 CYS A 356	25.640 24.584	19.676 19.943	20.263 19.679		22.08
ATOM ATOM	429		ALA A 357	26.228	18.483	20.160	1.00	22.51
MOTA	430	CA	ALA A 357	25.678	17.449 16.267	19.304 19.264		19.05 25.06
ATOM ATOM	431 432	CB C	ALA A 357 ALA A 357	26.606 24.296	17.048	19.778		20.99
MOTA	433	ŏ	ALA A 357	23.387	16.919	18.975		21.56
MOTA	434	N	ILE A 358	24.104 22.782	16.887 16.522	21.092 21.627		21.52 19.00
ATOM ATOM	435 436	CA CB	ILE A 358 ILE A 358	22.702	16.382	23.202	1.00	19.36
ATOM	437	CG2	ILE A 358	21.374	16.383	23.779		15.59 22.16
ATOM	438 439	CG1 CD1	ILE A 358 ILE A 358	23.623 24.073	15.153 15.174	23.614 25.079		23.75
ATOM ATOM	440	C	ILE A 358	21.747	17.597	21.291	1.00	18.17
MOTA	441	0	ILE A 358	20.590 22.171	17.322 18.843	20.947 21.443	1.00	17.46 22.77
MOTA MOTA	442 443	N CA	LYS A 359 LYS A 359	21.291	19.983	21.206	1.00	21.40
ATOM	444	CB	LYS A 359	21.931	21.234	21.809		23.15
ATOM	445	CG	LYS A 359 LYS A 359	22.175 20.879	21.133 20.855	23.334 24.063		24.28 24.08
ATOM ATOM	446 447	CD CE	LYS A 359	21.061	20.872	25.562	1.00	31.76
MOTA	448	NZ	LYS A 359	19.730	20.695	26.175 19.721	1.00	29.13 16.10
ATOM ATOM	449 450	C	LYS A 359 LYS A 359	20.925 19.764	20.166 20.377	19.721	1.00	20.28
ATOM	451	Ŋ	ILE A 360	21.914	20.094	18.841	1.00	15.62
MOTA	452	CA	ILE A 360	21.666 22.959	20.199 19.988	17.402 16.595		18.38 24.95
ATOM ATOM	453 454	CB CG2	ILE A 360 ILE A 360	22.659	19.672	15.136	1.00	28.87
ATOM	455	CG1	ILE A 360	23.846	21.221	16.659		25.71
MOTA	456	CD1 C	ILE A 360 ILE A 360	25.260 20.707	20.940 19.085	16.214 17.026		28.76 16.86
MOTA MOTA	457 458	0	ILE A 360	19.678	19.341	16.433	1.00	23.45
ATOM	459	N	THR A 361	20.986	17.861	17.467	1.00	17.32

ATOM	460	CA THR A	361	20.131	16.724	17.118	1.00	17.15
	461	CB THR A		20.647	15.411	17.703	1.00	21.09
ATOM		-		22.030	15.263	17.385		21.21
ATOM	462				14.207	17.146		23.13
ATOM	463	CG2 THR A		19.842				22.12
ATOM	464	C THR A		18.687	16.887	17.514		
ATOM	465	O THR A	361	17.786	16.414	16.813		22.98
ATOM	466	N GLU A	362	18.455	17.530	18.660		22.63
	467	CA GLU A		17.092	17.761	19.121	1.00	21.83
ATOM				17.076	18.335	20.541	1.00	25.44
ATOM	468			15.729	18.156	21.228		45.77
MOTA	469	CG GLU A	362			22.253		61.04
ATOM	470	CD GLU A		15.382	19.260			
MOTA	471	OE1 GLU A		16.281	19.648	23.059		67.71
MOTA	472	OE2 GLU A	362	14.199	19.723	22.249		58.48
ATOM	473	C GLU A		16.407	18.717	18.137		17.52
	474	O GLU A		15.226	18.567	17.836	1.00	18.31
MOTA				17.148	19.711	17.656	1.00	17.89
MOTA	475	N ALA A	303	16.613	20.652	16.656		22.83
ATOM	476	CA ALA A				16.358		21.95
ATOM	477	CB ALA A		17.624	21.753			
ATOM	478	C ALA A		16.304	19.896	15.348		21.89
ATOM	479	O ALA A	363	15.286	20.140	14.706		24.25
ATOM	480	N ILE A	364	17.196	18.994	14.952		23.12
ATOM	481	CA ILE A		16.995	18.214	13.715	1.00	23.74
				18.255	17.379	13.357	1.00	20.60
ATOM	482			17.943	16.320	12.288		20.36
MOTA	483	CG2 ILE A			18.329	12.855	1.00	16.57
MOTA	484	CG1 ILE A		19.349				17.77
ATOM	485	CD1 ILE A		20.748	17.766	12.820		
ATOM	486	C ILE A	364	15.709	17.382	13.705	1.00	28.19
ATOM	487	O ILE A	364	14.969	17.380	12.715	1.00	
ATOM	488	N GLN A		15.370	16.784	14.842	1.00	28.50
	489	CA GLN A		14.159	15.976	14.937	1.00	28.61
MOTA				14.049	15.352	16.309	1.00	34.56
MOTA	490	CB GLN A		15.324	14.645	16.719	1.00	
ATOM	491	CG GLN A					1.00	53.78
ATOM	492	CD GLN A		15.071	13.640	17.800		
ATOM	493	OE1 GLN A	365	13.968	13.106	17.901	1.00	
ATOM	494	NE2 GLN A	365	16.077	13.366	18.617		55.00
ATOM	495	C GLN A	365	12.893	16.737	14.620	1.00	
ATOM	496	O GLN A	365	11.919	16.145	14.172	1.00	30.81
	497		366	12.884	18.036	14.903	1.00	26.99
ATOM			366	11.733	18.889	14.598	1.00	23.20
ATOM	498			11.822	20.212	15.376	1.00	25.77
MOTA	499	CB TYR F				16.816	1 00	27.13
ATOM	500	CG TYR F	366	11.345	20.112			27.24
ATOM	501	CD1 TYR A		12.246	20.050	17.880	1.00	
ATOM	502	CE1 TYR A	366	11.787	19.956	19.198		32.73
ATOM	503	CD2 TYR F	366	9.984	20.075	17.103	1.00	29.26
ATOM	504	CE2 TYR A		9.521	19.976	18.402	1.00	33.96
	505	CZ TYR A		10.420	19.917	19.445	1.00	36.94
ATOM				9.925	19.808	20.729	1.00	45.77
ATOM	506	OH TYR A	300	11.743	19.165	13.084		22.71
MOTA	507	C TYR A	300		19.258	12.450	1 00	21.29
MOTA	508	O TYR A	366	10.688			1.00	23.15
ATOM	509	N VAL A		12.948	19.314	12.527		
MOTA	510	CA VAL A	¥ 367	13.130	19.536	11.085		25.23
ATOM	511	CB VAL A	367	14.586	19.907	10.742		22.53
ATOM	512	CG1 VAL A		14.798	19.914	9.224	1.00	20.69
	513	CG2 VAL A		14.878	21.280	11.292	1.00	17.32
MOTA		C VAL 2	367	12.650	18.303	10.281		28.13
ATOM	514			12.027	18.449	9.236		28.63
MOTA	515	O VAL	367			10.771		27.16
MOTA	516	N VAL	368	12.929	17.098			27.59
MOTA	517	CA VAL	A 368	12.450	15.890	10.116		
MOTA	518		368	13.048	14.606	10.759		23.81
ATOM	519	CG1 VAL A	A 368	12.340	13.380	10.226	1.00	29.32
ATOM	520	CG2 VAL	A 368	14.550	14.505	10.469		18.99
ATOM	521	C VAL	A 368	10.894	15.861	10.144	1.00	32.37
	522	O VAL	A 368	10.268	15.429	9.159	1.00	33.74
ATOM		M CITT	A 369	10.268	16.324	11.242		26.37
MOTA	523	N GLU	7 260	8.801	16.364	11.318		26.23
ATOM	524	CA GLU	A 369		16.756	12.712		29.58
MOTĄ	525	CB GLU	A 369	8.281	10.750	12.112	1.00	22.50

ATOM	526	CG	GLU A	369	8.304	15.647	13.763	1 00	33.78
ATOM	527	CD	GLU A	369	7.736	14.303	13.284	1.00	34.63
ATOM	528	OE1	GLU A	369	6.610	14.253	12.741	1.00	36.64
	529	OE2	GLU A		8.430	13.280	13.476	1.00	40.81
MOTA									
ATOM	530	C	GLU A	369	8.269	17.358	10.291	1.00	26.20
ATOM	531	0	GLU A	369	7.213	17.143	9.713	1.00	29.54
			PHE A		8.970	18.476	10.118	1.00	24.75
ATOM	532	И							
ATOM	533	CA	PHE A	370	8.607	19.475	9.114	1.00	24.70
ATOM	534	CB	PHE A	370	9.615	20.615	9.162	1.00	23.84
							8.093	1.00	24.23
MOTA	535	CG	PHE A		9.415	21.663			
ATOM	536	CD1	PHE A	370	8.265	22.444	8.071	1.00	24.20
ATOM	537	CD2	PHE A	370	10.415	21.918	7.161	1.00	24.12
						23.468	7.150	1.00	27.38
MOTA	538	CE1	PHE A		8.120	23.400			
ATOM	539	CE2	PHE A	370	10.276	22.943	6.234	1.00	26.73
ATOM	540	CZ	PHE A	370	9.125	23.722	6.231	1.00	24.57
	541	c	PHE A		8.648	18.805	7.712	1.00	26.16
MOTA									
MOTA	542	0	PHE A	370	7.666	18.841	6.966	1.00	24.95
ATOM	543	N	ALA A	371	9.780	18.172	7.395	1.00	25.24
ATOM	544	CA	ALA A		9.988	17.459	6.130	1.00	31.38
ATOM	545	CB	ALA A		11.281	16.681	6.171	1.00	27.13
ATOM	546	С	ALA A	371	8.829	16.525	5.794	1.00	33.49
ATOM	547	0	ALA A	371	8.328	16.550	4.674	1.00	35.75
					8.380	15.730	6.766	1.00	32.11
ATOM	548	N	LYS A						
ATOM	549	CA	LYS A		7.260	14.817	6.547	1.00	32.07
ATOM	550	CB	LYS A	372	7.025	13.969	7.780	1.00	31.18
-	551	CG	LYS A		8.142	13.030	8.132		34.27
ATOM									
MOTA	552	CD	LYS A		7.714	12.198	9.322		41.43
ATOM	553	CE	LYS A	372	8.898	11.535	9.996	1.00	47.18
ATOM	554	NZ	LYS A		8.490	10.731	11.203	1.00	52.21
					5.920	15.464	6.175		36.43
ATOM	555	C	LYS A				0.1/3		
MOTA	556	0	LYS A	372	5.047	14.804	5.612	1.00	39.27
ATOM	557	N	ARG A	373	5.742	16.735	6.511	1.00	38.37
ATOM	558	CA	ARG A		4.484	17.435	6.242	1.00	40.66
									45.55
ATOM	559	CB	ARG A		4.201	18.447	7.355	1.00	
ATOM	560	CG	ARG A	373	4.681	18.002	8.714		54.93
ATOM	561	CD	ARG A	373	3.682	17.131	9.441	1.00	59.22
	562	NE	ARG A		2.817	17.960	10.278		65.72
ATOM									
MOTA	563	cz	ARG A		2.860	17.988	11.607		63.53
ATOM	564	NH1	ARG A	373	3.723	17.222	12.261	1.00	61.86
ATOM	565	NH2	ARG A	373	2.057	18.802	12.281	1.00	66.65
	566	C	ARG A		4.503	18.179	4.916	1.00	41.35
ATOM									
MOTA	567	0	ARG A		3.496	18.773	4.516	1.00	40.31
MOTA	568	N	ILE A	374	5.669	18.203	4.271	1.00	41.14
ATOM	569	CA	ILE A	374	5.806	18.883	2.996	1.00	40.72
					7.237	19.329	2.697	1.00	36.14
MOTA	570	CB	ILE A						
ATOM	571	CG2	ILE A		7.298	19.939	1.299		32.36
MOTA	572	CG1	ILE A	374	7.675	20.387	3.702		34.12
ATOM	573	CD1	ILE A	374	9.159	20.603	3.712	1.00	36.75
			TTE 3	274	5.302	18.054	1.831		45.90
ATOM	574	C	ILE A	3/4					
MOTA	575	0	ILE A		5.733	16.929	1.583		42.19
ATOM	576	N	ASP A	375	4.301	18.625	1.183	1.00	50.81
ATOM	577	CA	ASP A		3.654	18.084	-0.002		52.36
						19.229			60.93
MOTA	578	CB	ASP A		2.859		-0.649		
MOTA	579	CG	ASP A	375	3.543	20.613	-0.449	1.00	68.87
ATOM	580	OD1	ASP A	375	4.421	20.987	-1.277	1.00	67.94
ATOM	581		ASP A		3.225	21.301	0.561		63.03
			ADE A	375					
MOTA	582	C	ASP A		4.690	17.547	-0.998		48.88
ATOM	583	0	ASP A	375	5.454	18.309	-1.595		48.00
ATOM	584	N	GLY A		4.743	16.234	-1.152	1.00	45.67
	585	CA	GLY A		5.683	15.669	-2.103		43.48
MOTA									
MOTA	586	C	GLY A		6.816	14.872	-1.514		40.36
ATOM	587	0	GLY A	376	7.200	13.837	-2.052	1.00	38.28
ATOM	588	N	PHE A	377	7.339	15.346	-0.394	1.00	37.97
ATOM	589	CA	PHE A		8.448	14.677	0.270		34.67
			בונות ב	377	8.826				34.08
MOTA	590	CB	PHE A			15.430	1.567		
MOTA	591	CG	PHE A	377	10.054	14.887	2.245	T.00	29.16

MOTA	592	CD1	PHE A 37	7	11.305	15.422	1.962	1.00 27.28
ATOM	593	CD2	PHE A 37	7	9.964	13.778	3.096	1.00 30.07
ATOM	594		PHE A 37		12.453	14.859	2.496	1.00 28.02
ATOM	595		PHE A 37		11.095	13.205	3.637	1.00 29.05
ATOM	596	CZ	PHE A 37	7	12.353	13.746	3.333	1.00 28.74
	597		PHE A 37		8.203	13.197	0.572	1.00 34.90
MOTA	598		PHE A 37		9.076	12.361	0.305	1.00 35.66
ATOM			MET A 37		7.060	12.871	1.169	1.00 34.38
ATOM	599		MET A 37		6.766	11.491	1.512	1.00 38.67
ATOM	600	CA	MET A 37	Ω Q	5.565	11.393	2.457	1.00 41.83
MOTA	601	CB	MET A 37	Ω	5.882	11.754	3.909	1.00 48.90
ATOM	602	CG	MET A 37	0	7.422	10.982	4.496	1.00 56.77
ATOM	603		MET A 37		6.884	9.291		1.00 57.67
MOTA	604	CE	MET A 37	0	6.574	10.586	0.301	1.00 42.95
ATOM	605	C	MET A 37	0	6.564	9.363	0.428	1.00 43.36
ATOM	606		GLU A 37	0	6.427	11.184	-0.877	1.00 44.95
MOTA	607	N			6.248	10.399	-2.086	1.00 45.80
MOTA	608	CA	GLU A 37		5.359	11.144	-3.071	1.00 52.39
MOTA	609	CB	GLU A 37	9	3.943	11.354	-2.587	1.00 61.32
MOTA	610	CG	GLU A 37		3.127	12.219	-3.537	1.00 71.44
MOTA	611	CD	GLU A 37	9	3.681	13.182	-4.126	1.00 73.32
MOTA	612	OE1		9	1.920	11.933	-3.693	1.00 77.96
MOTA	613	OE2	GLU A 37	9	7.581	10.057	-2.741	1.00 43.64
MOTA	614	C	GLU A 37		7.655	9.144	-3.553	1.00 43.83
MOTA	615	0	GLU A 37			10.794	-2.409	1.00 40.33
ATOM	616	N	LEU A 38	0	8.633 9.939	10.734	-2.986	1.00 40.49
ATOM	617	CA	LEU A 38		10.949	11.562	-2.536	1.00 39.57
MOTA	618	СВ	LEU A 38		10.949	12.909	-3.242	1.00 43.35
MOTA	619	CG	LEU A 38		9.660	13.313	-3.786	1.00 48.51
ATOM	620	CD1			11.496	13.947	-2.266	1.00 43.53
MOTA	621	CD2	LEU A 38	0	10.374	9.151	-2.509	1.00 43.17
ATOM	622	C	LEU A 38		9.702	8.546	-1.675	1.00 41.79
MOTA	623	0	CYS A 38		11.480	8.650	-3.053	1.00 46.89
MOTA	624	N	CYS A 38) 1 2 1	11.988	7.339	-2.651	1.00 51.11
ATOM	625	CA	CYS A 36) I	12.676	6.632	-3.838	1.00 48.63
ATOM	626 627	CB SG	CYS A 38		14.146	7.457	-4.487	1.00 48.71
MOTA	628	C	CYS A 38		12.938	7.479	-1.437	1.00 53.70
MOTA	629	Ö	CYS A 38	21	13.731	8.427	-1.357	1.00 54.89
ATOM	630	N	GLN A 38		12.813	6.559	-0.478	1.00 56.40
MOTA	631	CA	GLN A 38		13.625	6.552	0.747	1.00 57.37
ATOM ATOM	632	CB	GLN A 3		13.717	5.125	1.299	1.00 66.42
ATOM	633	CG	GLN A 3		14.527	4.981	2.596	1.00 80.23
ATOM	634	CD	GLN A 3		14.924	3.529	2.908	1.00 87.56
ATOM	635	OE1	GLN A 3		14.364	2.579	2.351	1.00 93.99
ATOM	636	NE2			15.916	3.361	3.781	1.00 90.30
ATOM	637	C	GLN A 3		15.030	7.108	0.529	1.00 52.28
ATOM	638	ō	GLN A 3		15.534	7.891	1.315	1.00 52.44
MOTA	639	N	ASN A 3	83	15.644	6.716	-0.571	1.00 48.24
ATOM	640	CA	ASN A 3	B3	16.975	7.166	-0.891	1.00 46.79
ATOM	641	CB	ASN A 3	B3	17.393	6.604	-2.241	1.00 55.14
ATOM	642	CG	ASN A 3	83	17.496	5.100	-2.232	1.00 63.92
ATOM	643	OD1	ASN A 3	83	18.603	4.559	-2.272	1.00 68.19
ATOM	644	ND2	ASN A 3	83	16.350	4.405	-2.198	1.00 65.25
MOTA	645	С	ASN A 3	83	17.000	8.669	-0.986	1.00 42.13
MOTA	646	0	ASN A 3	83	17.853	9.331	-0.408	1.00 38.96
MOTA	647	N	ASP A 3	84	16.064	9.203	-1.749	1.00 35.42 1.00 35.36
MOTA	648		ASP A 3		16.015	10.633	-1.945	1.00 35.36
ATOM	649		ASP A 3		15.137	10.984	-3.146	1.00 35.18
MOTA	650	CG	ASP A 3		15.790	10.618	-4.491 4.525	1.00 35.49
MOTA	651		ASP A 3	84	16.835	9.919	-4.525 -5.519	1.00 35.12
MOTA	652		ASP A 3	84	15.245		-0.701	1.00 34.33
MOTA	653		ASP A 3	84	15.578		-0.701	1.00 30.55
ATOM	654		ASP A 3	δ4 05	15.999	12.501 10.760	0.098	1.00 31.50
MOTA	655		GLN A 3	05 05	14.713 14.280		1.348	1.00 33.11
ATOM	656		GLN A 3	05 05	13.215		2.033	1.00 28.85
MOTA	657	CB	GLN A 3	03	13.413	10.311	2.000	

7 more	658	CG (GLN A 385	11.932	10.516	1.281	1.00	29.25
ATOM	659	CD (GLN A 385	10.981	9.578	1.942	1.00	35.13
MOTA	660		GLN A 385	11.392	8.704	2.711	1.00	39.80
MOTA	661		GLN A 385	9.703	9.737	1.663	1.00	34.78
MOTA	662		GLN A 385	15.488	11.552	2.277	1.00	31.53
MOTA			GLN A 385	15.751	12.632	2.816	1.00	29.68
MOTA	663		ILE A 386	16.251	10.466	2.394	1.00	29.20
ATOM	664		ILE A 386	17.452	10.430	3.208	1.00	31.16
ATOM	665		ILE A 386	17.992	8.987	3.310	1.00	30.97
ATOM	666		ILE A 386	19.411	8.959	3.925	1.00	29.51
ATOM	667		ILE A 386	16.982	8.148	4.103	1.00	
ATOM	668		ILE A 386	17.452	6.761	4.458	1.00	
ATOM	669		ILE A 386	18.518	11.411	2.696	1.00	
ATOM	670		ILE A 386	19.068	12.189	3.473	1.00	
ATOM	671		VAL A 387	18.788	11.400	1.392	1.00	
ATOM	672		VAL A 387	19.771	12.314	0.800	1.00	26.90
MOTA	673		VAL A 387	19.877	12.122	-0.763		25.37
ATOM	674		VAL A 387	20.555	13.328	-1.412	1.00	
ATOM	675		VAL A 387	20.658	10.864	-1.088		22.89
MOTA	676		VAL A 387	19.394	13.786	1.104		28.03
MOTA	677 678		VAL A 387	20.265	14.602	1.446	1.00	27.40
MOTA	679		LEU A 388	18.099	14.114	0.975	1.00	27.01
MOTA	680		LEU A 388	17.606	15.482	1.212	1.00	25.83
MOTA	681		LEU A 388	16.149	15.631	0.776	1.00	25.27
MOTA	682	CG	LEU A 388	15.822	15.597	-0.723	1.00	23.66
ATOM	683	CD1	LEU A 388	14.344	15.786	-0.898	1.00	24.29
MOTA	684		LEU A 388	16.587	16.686	-1.461	1.00	27.16
MOTA	685		LEU A 388	17.738	15.871	2.683	1.00	
ATOM ATOM	686		LEU A 388	18.094	16.998	2.998		25.91
ATOM	687		LEU A 389	17.461	14.928	3.572	1.00	25.45
ATOM	688		LEU A 389	17.578	15.192	4.994	1.00	
ATOM	689		LEU A 389	16.915	14.096	5.803		23.38
ATOM	690	CG	LEU A 389	15.402	14.206	5.789	1.00	
ATOM	691		LEU A 389	14.785	13.003	6.476	1.00	25.13
ATOM	692	CD2	LEU A 389	14.984	15.501	6.427		19.09
ATOM	693	c	LEU A 389	19.020	15.299	5.376	1.00	
ATOM	694	ŏ	LEU A 389	19.410	16.257	6.028		26.81
ATOM	695	N	LYS A 390	19.849	14.373	4.916		18.69
ATOM	696	CA	LYS A 390	21.250	14.429	5.273		21.34
ATOM	697	CB	LYS A 390	22.050	13.326	4.592		24.41
ATOM	698	CG	LYS A 390	21.938	11.960	5.200		29.06
ATOM	699	CD	LYS A 390	23.067	11.081	4.673		31.45
ATOM	700	CE	LYS A 390	23.062	9.718	5.342	1.00	40.63
ATOM	701	NZ	LYS A 390	24.240	8.890	4.933	1.00	46.61
ATOM	702	С	LYS A 390	21.884	15.751	4.907	1.00	25.73
MOTA	703	0	LYS A 390	22.706	16.287	5.644		26.32
MOTA	704	N	ALA A 391	21.478	16.295	3.770		25.48
MOTA	705	CA	ALA A 391	22.065	17.527	3.281	1.00	23.46
ATOM	706	CB	ALA A 391	22.076	17.505	1.766		26.48
MOTA	707	С	ALA A 391	21.401	18.795	3.750		20.95 27.25
MOTA	708	0	ALA A 391	22.074	19.789	4.005	1.00	21.07
MOTA	709	N	GLY A 392	20.082	18.773	3.838		
MOTA	710	CA	GLY A 392	19.349	19.965	4.202	1.00	22.76
MOTA	711	С	GLY A 392	18.923	20.133	5.638		23.17 20.90
ATOM	712	0	GLY A 392	18.420	21.184	5.972		23.99
MOTA	713	N	SER A 393	19.087	19.105	6.471		23.62
MOTA	714	CA	SER A 393	18.706	19.178	7.889		20.71
MOTA	715	CB	SER A 393	19.056	17.874	8.593		31.96
MOTA	716	OG	SER A 393	17.926	17.045	8.510	1.00	
MOTA	717	C	SER A 393	19.343	20.322	8.656 9.223	1.00	
MOTA	718	0	SER A 393	18.645	21.149		1.00	
MOTA	719	N	LEU A 394	20.670	20.332	8.677 9.365	1.00	
MOTA	720		LEU A 394	21.442	21.348 21.032	9.363		19.93
MOTA	721		LEU A 394	22.940		10.516		26.08
ATOM	722	CG	LEU A 394	23.831	20.918	10.310		21.54
MOTA	723	CD1	LEU A 394	25.207	21.380	70.700	1.00	22.24

PCT/EP03/04433 WO 03/093312

-43 -

								1 00 00 06
MOTA	724	CD2	LEU A	394	23.285	21.730	11.705	1.00 22.96 1.00 23.43
ATOM	725	С	LEU A	394	21.161	22.713	8.753 9.462	1.00 23.43
ATOM	726		LEU A		21.132	23.717 22.759	7.436	1.00 22.13
MOTA	727		GLU A		20.942 20.642	24.037	6.787	1.00 20.91
ATOM	728		GLU A		20.574	23.890	5.260	1.00 22.76
MOTA	729		GLU A		21.881	23.459	4.611	1.00 23.62
MOTA	730	CG	GLU A GLU A	393	21.809	23.461	3.084	1.00 26.69
ATOM	731	CD	GLU A	395	22.852	23.482	2.434	1.00 27.60
ATOM	732	OE1 OE2	GLU A	395	20.709	23.428	2.526	1.00 22.32
MOTA	733 734	C	GLU A	395	19.342	24.632	7.318	1.00 18.31
MOTA	735	ŏ	GLU A		19.270	25.832	7.574	1.00 20.03
ATOM ATOM	736	Ŋ	VAL A	396	18.311	23.810	7.498	1.00 18.03
ATOM	737	CA	VAL A	396	17.043	24.331	8.031	1.00 24.17
ATOM	738	CB	VAL A	396	15.891	23.342	7.818	1.00 20.05 1.00 18.41
ATOM	739	CG1	VAL A	396	14.587	23.854	8.517	1.00 18.41 1.00 22.83
ATOM	740		VAL A	396	15.663	23.177 24.744	6.288 9.525	1.00 25.12
MOTA	741	C	VAL A	. 396	17.174 16.476	25.639	10.006	1.00 26.40
MOTA	742	0	VAL A	396	18.077	24.073	10.232	1.00 23.34
MOTA	743	N	VAL A	. 397	18.358	24.401	11.617	1.00 18.37
ATOM	744	CA	VAL A		19.296	23.338	12.232	1.00 19.79
ATOM	745	CB	VAL A	397	19.915	23.829	13.534	1.00 20.93
ATOM	746 747	CGI	VAL A	397	18.517	22.069	12.472	1.00 16.14
ATOM ATOM	748	C	VAL A	397	19.006	25.802	11.635	1.00 17.79
ATOM	749	ŏ	VAL A	397	18.547	26.676	12.359	1.00 21.81
ATOM	750	N	PHE A	398	19.981	26.058	10.760	1.00 16.57
ATOM	751	CA	PHE A	398	20.625	27.355	10.735	1.00 12.50 1.00 16.85
ATOM	752	CB	PHE A	398	21.910	27.288	9.955 10.669	1.00 16.85 1.00 22.50
MOTA	753	CG	PHE A		23.017	26.588 26.899	11.986	1.00 22.50
MOTA	754	CD1			23.316 23.796	25.645	10.014	1.00 21.83
MOTA	755	CD2	PHE F	1 398	24.375	26.279	12.623	1.00 22.54
MOTA	756	CE1		7 338	24.859	25.021	10.652	1.00 23.29
<u>ATOM</u>	757	CE2 CZ	PHE A		25.151	25.334	11.953	1.00 22.58
ATOM	758 759	C	PHE A		19.718	28.486	10.249	1.00 19.24
ATOM ATOM	760	ŏ		A 398	19.944	29.669	10.570	1.00 19.14
ATOM	761	Ŋ	ILE A	A 399	18.663	28.138	9.513	1.00 20.43
ATOM	762	CA	ILE A	A 399	17.685	29.145	9.077	1.00 21.75 1.00 23.69
ATOM	763	CB		A 399	16.790	28.652	7.848	1.00 23.09
ATOM	764	CG2	ILE A	A 399	15.574	29.562	7.656 6.538	1.00 26.64
ATOM	765	CG1	. ILE	A 399	17.608 16.942	28.583 27.745	5.397	1.00 17.97
MOTA	766	CD1	. ILE	A 399	16.771	29.382	10.296	1.00 18.17
MOTA	767	C	TPR 1	A 399 A 399	16.484	30.507	10.662	1.00 20.59
MOTA	768 769	И О	ABC :	A 400	16.317	28.307	10.921	1.00 19.22
ATOM	770			A 400	15.451	28.415	12.087	1.00 20.62
ATOM ATOM	771			A 400	15.000	27.029	12.553	1.00 17.24
MOTA	772		ARG	A 400	13.783	26.537	11.852	1.00 15.74
ATOM	773		ARG .	A 400	13.420	25.143	12.246	1.00 17.01 1.00 21.84
ATOM	774	NE	ARG	A 400	12.189	24.760	11.553	1.00 21.38
MOTA	775	CZ	ARG	A 400	11.371	23.775 23.021	11.909 12.976	1.00 27.51
MOTA	776	NH.	L ARG	A 400	11.643 10.221	23.610	11.261	1.00 19.58
MOTA	777		2 ARG	A 400	16.132	29.177	13.235	1.00 22.12
ATOM	778			A 400 A 400	15.456		14.016	1.00 22.87
MOTA	779		MET	A 400 A 401	17.462		13.283	1.00 20.39
ATOM	780 781		MET	A 401	18.251		14.320	1.00 22.78
MOTA MOTA	782			A 401	19.740	29.612	14.026	1.00 21.38
ATOM	783		MET	A 401	20.681	30.082	15.096	1.00 17.22
MOTA	784		MET	A 401	22.356		14.524	1.00 24.87
MOTA	785		MET	A 401	22.858		14.579	1.00 30.52 1.00 27.16
ATOM	786	S C	MET	A 401	17.942		14.448 15.495	1.00 27.18
MOTA	787		MET	A 401	18.177 17.451		13.362	
ATOM	788		CYS	A 402	17.451		13.340	
MOTA	789	CA	CYS	A 402	11.102	33.321		

								•
7 5016	790	СВ	CYS A	102	16.827	33.801	11.911	1.00 34.97
ATOM	791		CYS A		18.382	33.864	11.142	1.00 54.57
ATOM			CYS A		15.947	33.699	14.236	1.00 33.06
ATOM	792				15.871	34.838	14.722	1.00 36.03
ATOM	793		CYS A		15.033	32.759	14.438	1.00 30.48
MOTA	794	N	ARG A	403		33.013	15.316	1.00 30.17
ATOM	795		ARG A		13.903		15.165	1.00 27.27
MOTA	796		ARG A		12.846	31.936		1.00 32.18
ATOM	797		ARG A		12.529	31.529	13.760	
MOTA	798	CD	ARG A	403	11.217	30.784	13.777	
ATOM	799	NE	ARG A	403	11.202	29.740	14.794	1.00 37.42
ATOM	800		ARG A		10.188	29.482	15.616	1.00 33.92
ATOM	801		ARG A	403	9.078	30.195	15.575	1.00 34.55
ATOM	802	NH2	ARG A	403	10.257	28.436	16.428	1.00 42.16
ATOM	803	C	ARG A	403	14.368	32.993	16.780	1.00 29.68
ATOM	804	ŏ	ARG A		13.653	33.472	17.649	1.00 30.31
	805	Ŋ	ALA A		15.556	32.431	17.016	1.00 26.70
MOTA	805	CA	ALA A		16.145	32.267	18.336	1.00 21.83
ATOM		CB	ALA A		16.328	30.768	18.612	1.00 17.43
ATOM	807		ALA A		17.490	32.962	18.394	1.00 23.99
MOTA	808	C			18.371	32.543	19.134	1.00 26.66
MOTA	809	0	ALA A		17.694	33.990	17.573	1.00 26.59
MOTA	810	N	PHE A		18.977	34.705	17.557	1.00 24.98
MOTA	811	CA	PHE A			34.470	16.227	1.00 18.47
MOTA	812	CB	PHE A		19.713	35.018	16.187	1.00 17.64
ATOM	813	CG	PHE A		21.110		16.313	1.00 16.69
MOTA	814	CD1	PHE A		22.202	34.177	15.956	1.00 19.09
ATOM	815		PHE A		21.345	36.370		1.00 19.09
ATOM	816	CE1	PHE A		23.514	34.669	16.199	
MOTA	817	CE2	PHE A		22.651	36.871	15.841	1.00 17.33 1.00 19.99
ATOM	818	CZ	PHE A		23.734	36.032	15.957	
ATOM	819	С	PHE A	405	18.765	36.197	17.805	1.00 28.98
ATOM	820	0	PHE A	405	17.845	36.789	17.256	1.00 31.78
ATOM	821	N	ASP A		19.581	36.763	18.703	1.00 31.70
ATOM	822	CA	ASP A		19.556	38.180	19.084	1.00 30.27
ATOM	823	CB	ASP A		19.786	38.339	20.598	1.00 30.55
ATOM	824	ĊĞ	ASP A		19.689	39.798	21.061	1.00 34.22
ATOM	825	OD1			19.722	40.747	20.278	1.00 31.76
	826	OD2			19.575	40.004	22.299	1.00 33.44
MOTA	827	C	ASP A		20.671	38.897	18.330	1.00 29.96
MOTA	828	ŏ	ASP A		21.821	38.953	18.804	1.00 29.82
MOTA	829	Ŋ	SER A		20.302	39.510	17.203	1.00 28.41
MOTA			SER A		21.263	40.224	16.374	1.00 34.69
MOTA	830	CA	SER A		20.597	40.719	15.093	1.00 37.05
ATOM	831	CB	SER A		21.531	40.766	14.018	1.00 51.86
MOTA	832	OG	SER A		21.922	41.381	17.115	1.00 34.14
MOTA	833	C			23.147	41.501	17.139	1.00 35.01
ATOM	834	0	SER A		21.113	42.206	17.764	1.00 38.76
MOTA	835	N	GLN A			43.345	18.519	1.00 40.20
MOTA	836	CA	GLN A		21.632	43.981	19.353	1.00 48.77
MOTA	837	CB	GLN A	408	20.516	44.338	18.577	1.00 63.31
MOTA	838	CG	GLN A	408	19.250		19.467	1.00 70.33
MOTA	839	CD	GLN A	408	18.001	44.400		1.00 73.70
ATOM	840	OE1	GLN A		17.761	45.387	20.175	1.00 72.43
MOTA	841	NE2			17.185	43.347	19.405	1.00 72.43
MOTA	842	С	GLN A	408	22.744	42.908	19.463	
MOTA	843	0	GLN A	408	23.827	43.493	19.484	1.00 36.77
ATOM	844	N	ASN A	409	22.514	41.803	20.156	1.00 32.86
MOTA	845	CA	ASN A	409	23.466	41.338	21.132	1.00 31.16
MOTA	846	CB	ASN A	409	22.722	41.083	22.438	1.00 34.90
ATOM	847	CG	ASN A	409	22.115	42.371	23.024	1.00 35.74
ATOM	848	OD1	ASN A	409	22.850	43.282	23.401	1.00 38.31
MOTA	849	MD2	ASN A	409	20.784	42.457	23.076	1.00 31.20
ATOM	850	C	ASN A	409	24.369	40.175	20.752	1.00 32.11
ATOM	851	ŏ	ASN A	409	25.179	39.729	21.574	1.00 34.18
	852	N	ASN A		24.291	39.743	19.494	1.00 29.63
ATOM	853	CA	ASN A	410	25.128	38.646	18.979	1.00 27.78
MOTA	854	CB	ASN A	410	26.597	39.063	18.877	1.00 24.50
MOTA	855 855	CG	ASN A		27.360	38.235	17.866	1.00 25.12
MOTA	055	<u> </u>	UPIN W					

ATOM	856	OD1	ASN A 410	26.851	37.955	16.780	1.00 29.04
ATOM	857	ND2	ASN A 410	28.568	37.813	18.224	1.00 27.47
ATOM	858	С	ASN A 410	25.016	37.476	19.928	1.00 28.72 1.00 27.57
MOTA	859	0	ASN A 410	26.016	36.970	20.457 20.020	1.00 27.68
MOTA	860	N	THR A 411	23.813	36.948 35.905	20.020	1.00 26.24
MOTA	861	CA	THR A 411	23.602 23.208	36.681	22.253	1.00 27.76
MOTA	862	CB	THR A 411	24.162	36.446	23.305	1.00 31.38
MOTA	863	OG1	THR A 411	21.784	36.514	22.604	1.00 16.40
MOTA	864	CG2	THR A 411 THR A 411	22.577	34.896	20.464	1.00 22.40
MOTA	865 866	C	THR A 411	21.649	35.282	19.779	1.00 24.61
MOTA	867	N	VAL A 412	22.768	33.612	20.771	1.00 20.76
MOTA MOTA	868	CA	VAL A 412	21.857	32.528	20.343	1.00 19.57
ATOM	869	CB	VAL A 412	22.607	31.487	19.475	1.00 19.83
ATOM	870		VAL A 412	21.655	30.780	18.524	1.00 18.01
ATOM	871	CG2	VAL A 412	23.691	32.130	18.740	1.00 33.67
ATOM	872	C	VAL A 412	21.278	31.708	21.508 22.411	1.00 18.12 1.00 23.18
MOTA	873	0	VAL A 412	22.009	31.325	21.453	1.00 25.10
MOTA	874	N	TYR A 413	19.990 19.320	31.386 30.575	22.465	1.00 17.45
ATOM	875	CA	TYR A 413	17.855	30.573	22.122	1.00 17.78
ATOM	876	CB	TYR A 413 TYR A 413	16.935	29.951	23.181	1.00 25.60
MOTA	877	CG CD1	TYR A 413	17.039	30.319	24.529	1.00 24.61
ATOM ATOM	878 879	CE1	TYR A 413	16.122	29.840	25.472	1.00 21.19
ATOM	880	CD2	TYR A 413	15.906	29.103	22.819	1.00 24.64
ATOM	881	CE2	TYR A 413	14.991	28.629	23.739	1.00 26.94
MOTA	882	CZ	TYR A 413	15.097	28.993	25.065	1.00 28.21
ATOM	883	OH	TYR A 413	14.145	28.487	25.945	1.00 27.94
ATOM	884	С	TYR A 413	19.906	29.164	22.453	1.00 23.48 1.00 24.97
ATOM	885	0	TYR A 413	19.656	28.401	21.518 23.488	1.00 22.58
ATOM	886	N	PHE A 414	20.684	28.828 27.534	23.400	1.00 21.94
MOTA	887	CA	PHE A 414	21.360 22.835	27.534	23.195	1.00 18.84
ATOM	888	CB	PHE A 414 PHE A 414	23.734	26.507	23.555	1.00 23.28
ATOM	889	CG CD1		23.637	25.283	22.871	1.00 23.77
ATOM ATOM	890 891	CD2		24.718	26.634	24.556	1.00 20.51
ATOM	892	CE1		24.510	24.201	23.178	1.00 25.81
ATOM	893	CE2		25.586	25.569	24.865	1.00 17.09
MOTA	894	CZ	PHE A 414	25.483	24.350	24.178	1.00 23.54
ATOM	895	С	PHE A 414	21.303	26.977	25.057	1.00 25.66 1.00 22.04
MOTA	896	0	PHE A 414	21.612	27.677	26.024 25.196	1.00 25.08
MOTA	897	N	ASP A 415	20.866 20.849	25.731 25.114	26.513	1.00 22.21
MOTA	898	CA	ASP A 415	22.303	24.853	26.921	1.00 17.07
ATOM	899	CB CG	ASP A 415 ASP A 415	22.441	23.735	27.894	1.00 18.13
ATOM	900 901		ASP A 415	21.457	23.014	28.110	1.00 18.33
ATOM ATOM	902	ODS	ASP A 415	23.551	23.579	28.420	1.00 20.42
ATOM	903	C	ASP A 415	20.130	25.970	27.579	1.00 25.14
ATOM	904	ō	ASP A 415	20.700	26.259	28.633	1.00 29.15
ATOM	905	N	GLY A 416	18.912	26.408	27.269	1.00 20.65
ATOM	906	CA	GLY A 416	18.118	27.176	28.201	1.00 18.89 1.00 13.58
MOTA	907	C	GLY A 416	18.258	28.682	28.257 28.744	1.00 13.33
MOTA	908	0	GLY A 416	17.349	29.327 29.254	27.817	1.00 14.55
MOTA	909	N	LYS A 417	19.364 19.498	30.716	27.861	1.00 18.31
ATOM	910	CA	LYS A 417 LYS A 417	20.345	31.134	29.074	1.00 20.71
MOTA	911	CB CG	LYS A 417	19.682	30.877	30.428	1.00 22.06
MOTA MOTA	912 913	CD	LYS A 417	20.679	31.167	31.538	1.00 23.89
ATOM	914	CE	LYS A 417	19.970	31.232	32.891	1.00 26.28
ATOM	915		LYS A 417	20.937	31.696	33.916	1.00 27.48
ATOM	916	C	LYS A 417	20.183	31.202	26.592	1.00 23.82
ATOM	917	0	LYS A 417	20.635	30.382	25.781	1.00 21.77
ATOM	918		TYR A 418	20.315	32.526	26.443 25.270	1.00 21.57 1.00 19.31
MOTA	919		TYR A 418	20.972	33.115 34.492	25.270	1.00 19.31
MOTA	920		TYR A 418	20.369 19.066		24.321	1.00 21.12
ATOM	921	CG	TYR A 418	T3.000	J4.4U/	24.142	

ATOM	922	CD1	TYR A	418	17.856	34.087	24.777	1.00	18.03
ATOM	923	CE1	TYR A		16.682	33.930	24.048		22.16
ATOM	924	CD2	TYR A		19.060	34.576	22.743		19.41
MOTA	925	CE2	TYR A	418	17.903	34.419	22.007		16.83
MOTA	926	CZ	TYR A		16.728	34.099	22.648		24.12
MOTA	927	OH	TYR A		15.601	33.944	21.890		22.47 19.85
MOTA	928	C	TYR A		22.471 22.974	33.183 33.820	25.451 26.385		25.51
MOTA	929	O	TYR A ALA A		23.180	32.482	24.570	1.00	16.24
ATOM ATOM	930 931	N CA	ALA A		24.630	32.365	24.577	1.00	15.65
ATOM	932	CB	ALA A		24.986	30.903	24.326		17.04
MOTA	933	C	ALA A		25.463	33.245	23.629	1.00	25.93
MOTA	934	Ö	ALA A		25.168	33.359	22.432		27.89
ATOM	935	N	SER A		26.540	33.817	24.157	1.00	23.17
ATOM	936	CA	SER A		27.455	34.619	23.360	1.00	
ATOM	937	СВ	SER A		28.202	35.577	24.280 25.170	1.00	27.55 31.44
ATOM	938	OG C	SER A SER A		29.050 28.442	34.861 33.622	22.735		25.61
ATOM ATOM	939 940	C O	SER A		28.462	32.461	23.132	1.00	
ATOM	941	И	PRO A		29.267	34.040	21.748	1.00	
ATOM	942	CD	PRO A		29.281	35.313	20.998	1.00	28.16
ATOM	943	CA	PRO A	421	30.209	33.071	21.160	1.00	
ATOM	944	CB	PRO A	421	31.014	33.928	20.178	1.00	
MOTA	945	CG	PRO A		30.031	34.959	19.743		24.69
ATOM	946	C	PRO A		31.158	32.380	22.163 21.988		34.03 31.00
ATOM	947	0	PRO A ASP A		31.509 31.627	31.199 33.142	23.158		33.32
ATOM	948 949	N CA	ASP A		32.570	32.623	24.154		35.81
ATOM ATOM	950	CB	ASP A		33.136	33.742	25.030		44.04
ATOM	951	CG	ASP A		32.246	34.946	25.069		54.68
ATOM	952		ASP A		32.454	35.892	24.251		54.42
ATOM	953	OD2			31.327	34.920	25.913		58.40
MOTA	954	С	ASP A		32.104	31.415	24.972	1.00	
MOTA	955	0	ASP A		32.923	30.698	25.550	1.00	29.48
ATOM	956	N	VAL A		30.796 30.197	31.180 30.031	24.968 25.620	1.00	
ATOM	957 958	CA CB	VAL A		28.671	30.120	25.495	1.00	
MOTA MOTA	959		VAL A		28.025	28.771	25.617	1.00	20.56
ATOM	960	CG2			28.115	31.068	26.536	1.00	21.12
ATOM	961	C	VAL A		30.724	28.783	24.894	1.00	
MOTA	962	0	VAL A		30.975	27.746	25.499	1.00	
MOTA	963	N	PHE A		31.040	28.951	23.611	1.00	
MOTA	964	CA	PHE A		31.507	27.854 27.963	22.774 21.371	1.00 1.00	
ATOM	965	CB CG	PHE A		30.860 29.341	28.011	21.371	1.00	
MOTA MOTA	966 967	CD1	PHE A		28.668	29.227	21.384	1.00	
ATOM	968		PHE A		28.598	26.843	21.509	1.00	15.76
ATOM	969	CE1	PHE A	404	27.290	29.270	21.500		16.18
ATOM	970	CE2	PHE A	424	27.238	26.880	21.623		13.58
ATOM	971	CZ	PHE A		26.573	28.099	21.624		16.90
MOTA	972	C	PHE A		33.014	27.757	22.663	1.00	23.66 24.93
ATOM	973	O	PHE A		33.539 33.727	26.929 28.552	21.911 23.451	1.00	
ATOM	974 975	N CA	LYS A LYS A		35.186	28.527	23.392	1.00	
ATOM ATOM	976	CB	LYS A		35.776	29.467	24.452		32.35
ATOM	977	CG	LYS A	425	37.306	29.529	24.457		31.98
ATOM	978	CD	LYS A		37.762	30.593	25.418	1.00	39.70
MOTA	979	CE	LYS A	425	39.265	30.718	25.450		48.00
ATOM	980	NZ	LYS A	425	39.725	31.844	26.336		53.67
MOTA	981	C	LYS A	425	35.889	27.157	23.476	1.00	31.57 27.27
ATOM	982	O NT	LYS A SER A	425 426	36.792 35.521	26.863 26.339	22.673 24.465		30.78
ATOM ATOM	983 984	N CA	SER A		36.182	25.050	24.403		33.82
ATOM	985	CB	SER A		35.862	24.390	25.959		30.28
ATOM	986	OG	SER A	426	34.486	24.161	26.133		37.92
MOTA	987	C	SER A	426	35.992	24.104	23.417	1.00	35.48

7 CIOM	988	O SER A	426	36.713	23.122	23.286	1.00	37.65
MOTA MOTA	989	N LEU A		35.109	24.463	22.488	1.00	35.14
ATOM	990	CA LEU A		34.879	23.644	21.300	1.00	33.29
ATOM	991	CB LEU A		33.771	24.270	20.461		30.08
	992	CG LEU A		32.682	23.462	19.781	1.00	28.00
MOTA	993	CD1 LEU A		32.151	22.380	20.671		25.88
ATOM	994	CD2 LEU A		31.574	24.418	19.397		25.10
MOTA		C LEU A		36.166	23.655	20.494		33.91
MOTA	995			36.533	22.656	19.901		36.72
MOTA	996			36.862	24.790	20.503		39.65
ATOM	997	N GLY A		38.105	24.932	19.750		40.93
ATOM	998 999	C GLY A		37.884	25.241	18.269		43.39
MOTA	1000	O GLY A		38.806	25.108	17.455		42.81
MOTA		N CYS A	129	36.670	25.685	17.927		43.35
ATOM	1001 1002	CA CYS A	429	36.291	25.995	16.544		43.84
MOTA	1002	CB CYS A	129	35.025	25.224	16.176	1.00	43.95
ATOM	1003	SG CYS A	129	35.244	23.452	16.181	1.00	50.28
MOTA	1004	C CYS A		36.012	27.475	16.409		42.57
MOTA	1005	O CYS A		35.003	27.873	15.838		39.45
MOTA	1007	N GLU A		36.934	28.292	16.901		43.43
MOTA	1007	CA GLU A		36.761	29.740	16.874	1.00	45.32
MOTA	1008	CB GLU A		38.051	30.447	17.301		53.81
ATOM ATOM	1010	CG GLU A		38.849	29.738	18.439	1.00	70.87
ATOM	1011	CD GLU A		38.051	29.456	19.737	1.00	77.73
ATOM	1011	OE1 GLU A		37.138	30.245	20.098		80.51
ATOM	1012	OE2 GLU A		38.365	28.437	20.408		78.46
ATOM	1013	C GLU A		36.236	30.320	15.552		40.15
ATOM	1015	O GLU A		35.304	31.127	15.563		35.32
ATOM	1016	N ASP A		36.782	29.870	14.420		36.97
ATOM	1017	CA ASP A		36.355	30.383	13.101	1.00	37.50
ATOM	1018	CB ASP A		37.352	30.007	12.009		45.12
ATOM	1019	CG ASP A		38.743	30.507	12.303		50.38
ATOM	1020	OD1 ASP A		39.005	31.715	12.088	1.00	52.92
ATOM	1021	OD2 ASP A		39.564	29.686	12.767		58.71
ATÖM	1022	C ASP A		34.953	29.983	12.668		31.17
ATOM	1023	O ASP A		34.169	30.832	12.249	1.00	29.39
ATOM	1024	N PHE A		34.642	28.697	12.805		25.82
ATOM	1025	CA PHE A	432	33.334	28.162	12.467		24.06
ATOM	1026	CB PHE A	432	33.343	26.640	12.666		23.24
ATOM	1027	CG PHE A		31.981	26.008	12.634		26.00
ATOM	1028	CD1 PHE A	432	31.359	25.728	11.428		24.09
ATOM	1029	CD2 PHE A		31.301	25.727	13.826	1.00	24.00
MOTA	1030	CE1 PHE A		30.077	25.182	11.407		25.60
MOTA	1031	CE2 PHE A		30.017	25.182	13.819		23.27
MOTA	1032	CZ PHE A		29.399	24.907	12.608	1.00	27.15
MOTA	1033	C PHE A	432	32.290	28.823	13.368		24.49
MOTA	1034	O PHE A	432	31.166		12.939 14.614	1.00	23.40 23.33
MOTA	1035	N ILE A	433	32.667	29.123			23.33
MOTA	1036	CA ILE A	433	31.729	29.746	15.545		24.82
ATOM	1037	CB ILE A	433	32.226	29.697	17.038 17.946		24.79
ATOM	1038	CG2 ILE A		31.307	30.551	17.554		22.78
ATOM	1039	CG1 ILE A		32.233	28.244 27.630	17.534		21.04
ATOM	1040	CD1 ILE A	433	30.846				17.19
ATOM	1041	C ILE A	433	31.453	31.179 31.589	15.113 15.046		21.19
ATOM	1042	O ILE A	433	30.293	31.389	14.770	1 00	23.08
ATOM	1043	N SER A	434	32.491	33.319	14.770		25.60
ATOM	1044	CA SER A	434	32.257 33.561	34.097	14.162		28.06
ATOM	1045	CB SER A			33.294	13.558		37.81
ATOM	1046	OG SER A		34.547 31.465	33.276	13.028		23.82
ATOM	1047	C SER A O SER A		30.564	34.072	12.821		23.76
MOTA	1048			31.752	32.279	12.199		24.82
ATOM	1049		435 435	31.034	32.096	10.947	1.00	
ATOM	1050	CA PHE A CB PHE A	435	31.646	30.923	10.161		26.80
ATOM	1051 1052	CG PHE A	435	31.106	30.767	8.748		30.19
ATOM	1052	CD1 PHE A		30.205	31.686	8.209		35.50
MOTA	T022	CDT EIID W	100					-

		-	
	A	o	
_	4	ж.	_

						00 670	7 061	1.00 33.97
MOTA	1054	CD2	PHE A	135	31.487	29.678	7.961	1.00 33.97
ATOM	1055	CE1	PHE A	135	29.684	31.523	6.906	1.00 34.39
	1056		PHE A		30.977	29.505	6.657	1.00 34.83
ATOM			PHE A		30.074	30.430	6.136	1.00 31.71
MOTA	1057	CZ	PRE A	±33		31.844	11.264	1.00 26.45
ATOM	1058	С	PHE A		29.548			1.00 28.86
MOTA	1059	0	PHE A		28.665	32.480	10.688	
ATOM	1060	N	VAL A	436	29.255	30.967	12.223	1.00 22.48
ATOM	1061	CA	VAL A		27.865	30.691	12.559	1.00 17.41
	1062	CB	VAL A		27.757	29.624	13.695	1.00 17.64
ATOM			VAL A		26.377	29.570	14.228	1.00 22.49
ATOM	1063	CGT	VAL A	426	28.122	28.278	13.195	1.00 17.15
ATOM	1064		VAL A	436			12.991	1.00 17.44
ATOM	1065	С	VAL A		27.164	31.978		
ATOM	1066	0	VAL A	436	26.053	32.278	12.534	
ATOM	1067	N	PHE A	437	27.803	32.741	13.874	1.00 19.96
ATOM	1068	CA	PHE A	437	27.184	33.971	14.362	1.00 22.62
ATOM	1069	CB	PHE A	437	27.946	34.539	15.573	1.00 24.58
	1070	CG	PHE A		27.559	33.905	16.891	1.00 23.31
ATOM					27.912	32.593	17.180	1.00 24.58
MOTA	1071		PHE A	437		34.627	17.841	1.00 23.23
ATOM	1072	CD2	PHE A		26.855			1.00 22.25
ATOM	1073	CE1			27.572	32.012	18.402	
ATOM	1074	CE2	PHE A	437	26.514	34.055	19.059	1.00 23.56
ATOM	1075	CZ	PHE A	437	26.874	32.746	19.334	1.00 18.83
MOTA	1076	Č	PHE A		27.010	35.034	13.274	1.00 22.54
		ŏ	PHE A	437	25.985	35.716	13.232	1.00 27.26
MOTA	1077		GLU A		28.001	35.176	12.400	1.00 26.36
ATOM	1078	N			27.898	36.157	11.302	1.00 27.43
MOTA	1079	CA	GLU A				10.440	1.00 30.05
ATOM	1080	CB	GLU A		29.164	36.179		1.00 31.17
MOTA	1081	CG	GLU A	438	29.073	37.131	9.227	
ATOM	1082	CD	GLU A	438	30.417	37.447	8.605	1.00 31.35
ATOM	1083	OE1	GLU A	438	31.384	36.685	8.801	1.00 27.62
ATOM	1084	OE2			30.509	38.491	7.932	1.00 40.19
		C	GLU A		26.674	35.839	10.450	1.00 25.73
MOTA	1085		GLU A		25.918	36.730	10.093	1.00 28.14
ATOM	1086	0			26.449	34.555	10.188	1.00 26.08
MOTA	1087	N	PHE A				9.433	1.00 24.60
ATOM	1088	CA	PHE A		25.292	34.118		1.00 26.02
ATOM	1089	СВ	PHE A		25.398	32.619	9.135	
MOTA	1090	CG	PHE A	439	24.280	32.098	8.283	1.00 27.70
ATOM	1091	CD1	PHE A	439	24.304	32.270	6.904	1.00 29.06
MOTA	1092	CD2		439	23.177	31.483	8.855	1.00 31.10
MOTA	1093	CE1		439	23.251	31.842	6.123	1.00 24.89
	1094	CE2			22.111	31.050	8.069	1.00 31.13
ATOM			PHE A		22.153	31.234	6.701	1.00 28.01
ATOM	1095	CZ			23.964	34.426	10.162	1.00 28.45
MOTA	1096	C	PHE A		23.904		9.518	1.00 28.20
MOTA	1097	0	PHE A		22.958	34.770		1.00 26.29
ATOM	1098	N	GLY A		23.926	34.257	11.491	
ATOM	1099	CA	GLY A	440	22.699	34.550	12.217	1.00 20.95
ATOM	1100	С	GLY A	440	22.380	36.035	12.079	1.00 24.76
ATOM	1101	Ō	GLY A		21.247	36.459	11.831	1.00 24.56
ATOM	1102	Ň	LYS A		23.409	36.842	12.249	1.00 25.11
			LYS A	111	23.283	38.290	12.135	1.00 31.81
ATOM	1103	CA.	THO A	441	24.674	38.871	12.293	1.00 34.53
MOTA	1104	CB	LYS A			40.343	12.482	1.00 48.07
MOTA	1105	CG	LYS A		24.720			1.00 58.50
ATOM	1106	CD	LYS A		25.618	40.643	13.668	1.00 61.35
MOTA	1107	CE	LYS A		25.088	39.955	14.934	
ATOM	1108	NZ	LYS A	441	25.698	40.550	16.152	1.00 67.81
ATOM	1109	С	LYS A	441	22.741	38.659	10.733	1.00 34.70
ATOM	1110	ŏ	LYS A		21.767	39.411	10.579	1.00 32.85
	1111	N	SER A		23.408	38.091	9.729	1.00 33.69
MOTA			SER A		23.113	38.278	8.312	1.00 32.10
ATOM	1112	CA	A Aug	442	24.060	37.413	7.493	1.00 34.00
ATOM	1113	CB	SER A				6.142	1.00 42.63
ATOM	1114	OG	SER A		23.706	37.415		1.00 42.05
MOTA	1115	C	SER A		21.699	37.939	7.953	
ATOM	1116	0	SER A		21.022	38.710	7.283	1.00 28.07
MOTA	1117	N	LEU A	443	21.252	36.769	8.383	1.00 30.75
ATOM	1118	CA	LEU A	443	19.903	36.341	8.091	1.00 28.97
ATOM	1119	CB	LEU A	443	19.754	34.844	8.362	1.00 32.66
111 011								

						7 005	1.00 34.63
ATOM	1120	CG	LEU A 443	19.232	33.966	7.225	
ATOM	1121	CD1	LEU A 443	19.001	32.579	7.758	1.00 34.61
MOTA	1122	CD2	LEU A 443	17.933	34.502	6.669	1.00 35.80
	1123		LEU A 443	18.900	37.163	8.897	1.00 33.40
MOTA			LEU A 443	17.761	37.366	8.461	1.00 31.79
MOTA	1124	0	DEO W 442	19.330	37.656	10.063	1.00 39.70
ATOM	1125		CYS A 444		38.478	10.937	1.00 44.50
MOTA	1126	CA	CYS A 444	18.474			1.00 50.28
MOTA	1127	CB	CYS A 444	19.117	38.687	12.312	1.00 50.26
ATOM	1128	SG	CYS A 444	18.752	37.411	13.539	1.00 54.66
ATOM	1129	C	CYS A 444	18.177	39.845	10.346	1.00 44.03
	1130	ŏ	CYS A 444	17.053	40.343	10.468	1.00 42.14
ATOM		-	SER A 445	19.190	40.456	9.733	1.00 43.30
MOTA	1131	N	SER A 445	19.020	41.765	9.118	1.00 47.44
MOTA	1132	CA		20.343	42.266	8.518	1.00 48.13
ATOM	1133	CB	SER A 445	20.343	41.518	7.383	1.00 50.15
MOTA	1134	OG	SER A 445	20.752			1.00 48.45
ATOM	1135	С	SER A 445	17.885	41.815	8.071	
MOTA	1136	0	SER A 445	17.459	42.901	7.663	1.00 53.44
ATOM	1137	Ŋ	MET A 446	17.393	40.656	7.636	1.00 44.69
	1138	CA	MET A 446	16.306	40.631	6.665	1.00 43.05
ATOM			MET A 446	16.389	39.386	5.789	1.00 40.50
MOTA	1139	CB		17.577	39.419	4.842	1.00 41.60
MOTA	1140	CG	MET A 446		37.906	3.917	1.00 47.28
MOTA	1141	SD	MET A 446	17.833			1.00 42.50
ATOM	1142	CE	MET A 446	19.506	37.667	4.191	
ATOM	1143	С	MET A 446	14.953	40.725	7.355	1.00 46.65
MOTA	1144	0	MET A 446	13.971	41.150	6.746	1.00 50.18
ATOM	1145	N	HIS A 447	14.921	40.382	8.643	1.00 46.34
	1146	CA	HIS A 447	13.702	40.426	9.420	1.00 48.76
MOTA			HIS A 447	13.259	41.882	9.589	1.00 60.69
MOTA	1147	CB		12.149	42.066	10.578	1.00 78.35
MOTA	1148	CG	HIS A 447		41.273	11.592	1.00 83.48
MOTA	1149	CD2	HIS A 447	11.722			1.00 85.45
MOTA	1150	ND1	HIS A 447	11.308	43.163	10.569	
ATOM	1151	CE1	HIS A 447	10.405	43.032	11.529	1.00 86.49
ATOM	1152	NE2	HIS A 447	10.633	41.893	12.161	1.00 87.93
	1153	C	HIS A 447	12.618	39.583	8.729	1.00 47.17
MOTA			HIS A 447	11.618	40.114	8.233	1.00 48.76
ATŌM	1154	Ō	LEU A 448	12.853	38.272	8.654	1.00 43.85
MOTA	1155	N		11.922	37.320	8.021	1.00 37.21
MOTA	1156	CA	LEU A 448		36.021	7.633	1.00 36.92
ATOM	1157	CB	LEU A 448	12.667		6.867	1.00 36.45
MOTA	1158	CG	LEU A 448	14.004	36.045		1.00 35.34
ATOM	1159	CD1	LEU A 448	14.486	34.629	6.601	
ATOM	1160	CD2	LEU A 448	13.867	36.798	5.553	1.00 41.17
ATOM	1161	C	LEU A 448	10.703	36.961	8.887	1.00 34.64
	1162	ŏ	LEU A 448	10.847	36.731	10.083	1.00 35.66
MOTA		И	THR A 449	9.512	36.911	8.288	1.00 31.11
MOTA	1163		THR A 449	8.305	36.549	9.033	1.00 28.99
MOTA	1164	CA		7.006	36.973	8.313	1.00 30.22
MOTA	1165	CB	THR A 449		36.098	7.201	1.00 29.38
ATOM	1166		THR A 449	6.777		7.839	
MOTA	1167	CG2	THR A 449	7.081	38.431	7.039	1.00 29.64
ATOM	1168	С	THR A 449	8.271	35.030	9.134	1.00 29.04
MOTA	1169	0	THR A 449	8.953	34.351	8.371	1.00 31.91
MOTA	1170	N	GLU A 450	7.479	34.491	10.051	1.00 26.47
	1171	CA	GLU A 450	7.392	33.047	10.182	1.00 27.53
ATOM			GLU A 450	6.328	32.679	11.204	1.00 25.91
MOTA	1172	CB	GLU A 450	6.730	33.026	12.617	1.00 27.73
MOTA	1173	CG	GLU A 450		32.146	13.117	1.00 24.37
MOTA	1174	CD	GLU A 450	7.853			1.00 29.52
MOTA	1175	OE1	GLU A 450	7.554	31.004	13.513	1.00 29.32
ATOM	1176	OE2		9.021	32.586	13.108	
ATOM	1177	C	GLU A 450	7.104	32.350	8.844	1.00 29.72
ATOM	1178	ŏ	GLU A 450	7.748	31.372	8.492	1.00 29.06
	1179	N	ASP A 451	6.181	32.899	8.070	1.00 32.63
MOTA		CA	ASP A 451	5.830		6.780	1.00 30.31
MOTA	1180		ASP A 451	4.615		6.182	1.00 34.34
ATOM	1181	CB		3.314		6.891	1.00 39.42
ATOM	1182	CG	ASP A 451			7.755	1.00 42.60
MOTA	1183		L ASP A 451	3.330		6.573	1.00 46.92
ATOM	1184		2 ASP A 451	2.261	33.254		1.00 27.29
MOTA	1185	С	ASP A 451	7.005	32.321	5.813	1.00 21.29

ATOM	1186	0	ASP A	451	7.238	31.364	5.090	1.00 27.40
ATOM	1187	N	GLU A		7.765	33.404	5.821	1.00 29.17
ATOM	1188	CA	GLU A		8.928	33,510	4.946	1.00 33.64
	1189	CB	GLU A		9.521	34.927	5.022	1.00 34.38
ATOM		CG	GLU A		8.592	35.990	4.410	1.00 38.12
MOTA	1190				9.061	37.426	4.609	1.00 40.47
MOTA	1191	CD	GLU A	454			5.330	1.00 42.73
MOTA	1192		GLU A	452	10.047	37.667		
ATOM	1193	OE2	GLU A		8.424	38.339	4.047	1.00 45.30
ATOM	1194	C	GLU A	452	9.976	32.432	5.286	1.00 35.02
ATOM	1195	0	GLU A	452	10.558	31.814	4.378	1.00 32.26
ATOM	1196	N	ILE A	453	10.200	32.209	6.589	1.00 31.95
ATOM	1197	CA	ILE A		11.159	31.194	7.061	1.00 28.64
ATOM	1198	CB	ILE A		11.397	31.290	8.615	1.00 31.75
	1199	CG2	ILE A	453	12.135	30.045	9.139	1.00 28.09
ATOM			ILE A		12.218	32.538	8.952	1.00 29.57
ATOM	1200	CG1			12.224	32.863	10.422	1.00 27.64
ATOM	1201	CD1	ILE A			29.793	6.707	1.00 25.34
MOTA	1202	С	ILE A		10.640			1.00 27.62
ATOM	1203	0	ILE A		11.408	28.904	6.331	
ATOM	1204	N	ALA A		9.331	29.604	6.834	1.00 25.41
ATOM	1205	CA	ALA A		8.698	28.317	6.524	1.00 28.05
MOTA	1206	CB	ALA A	454	7.194	28.381	6.798	1.00 23.33
MOTA	1207	С	ALA A	454	8.941	27.940	5.064	1.00 30.98
ATOM	1208	Ō	ALA A		9.408	26.839	4.763	1.00 27.28
ATOM	1209	N	LEU A		8.696	28.899	4.173	1.00 34.22
ATOM	1210	CA	LEU A		8.850	28.677	2.744	1.00 33.15
	1211	CB	LEU A		8.023	29.706	1.945	1.00 35.88
MOTA	1212		LEU A		6.504	29.399	1.973	1.00 35.93
MOTA		CG			5.706	30.626	1.672	1.00 39.84
MOTA	1213	CD1			6.159	28.277	0.989	1.00 32.00
MOTA	1214	CD2					2.328	1.00 30.16
ATOM	1215	С	LEU A		10.307	28.601		1.00 30.10
MOTA	1216	0	LEU A		10.676	27.724	1.540	
MOTA	1217	N	PHE A		11.150	29.460	2.894	1.00 26.03
ATOM	1218	CA	PHE A		12.564	29.400	2.561	1.00 25.28
ATOM	1219	CB	PHE A		13.313	30.595	3.142	1.00 27.10
MOTA	1220	CG	PHE A		14.766	30.654	2.734	1.00 32.50
MOTA	1221	CD1	PHE A	456	15.151	30.366	1.421	1.00 31.72
MOTA	1222	CD2	PHE A	456	15.754	30.994	3.660	1.00 32.12
MOTA	1223	CE1	PHE A	456	16.484	30.414	1.040	1.00 31.33
ATOM	1224	CE2	PHE A	456	17.097	31.046	3.285	1.00 34.09
ATOM	1225	CZ	PHE A	456	17.465	30.755	1.971	1.00 33.73
ATOM	1226	C	PHE A		13.165	28.073	3.061	1.00 27.08
ATOM	1227	ŏ	PHE A		14.077	27.522	2.452	1.00 24.18
ATOM	1228	Ň	SER A		12.626	27.547	4.162	1.00 26.66
ATOM	1229	CA	SER A		13.084	26.278	4.719	1.00 24.70
	1230	CB	SER A		12.366	25.986	6.034	1.00 22.68
MOTA	1231	OG	SER A		12.761	26.899	7.025	1.00 28.15
MOTA			SER A		12.734	25.169	3.748	1.00 23.81
ATOM	1232	C	SER A		13.561	24.315	3.425	1.00 21.55
MOTA	1233	0			11.470	25.154	3.337	1.00 24.49
ATOM	1234	N	ALA A			24.142	2.397	1.00 27.62
MOTA	1235	CA	ALA A		10.992			1.00 26.08
MOTA	1236	CB	ALA A		9.526	24.345	2.126	
MOTA	1237	C	ALA A		11.811	24.190	1.095	1.00 25.57
ATOM	1238	0	ALA A		12.205	23.161	0.571	1.00 28.96
ATOM	1239	N	PHE A	459	12.153	25.399	0.660	1.00 27.37
MOTA	1240	CA	PHE A		12.945	25.642	-0.553	1.00 28.58
MOTA	1241	CB	PHE A		13.083	27.162	-0.758	1.00 28.53
ATOM	1242	CG	PHE A		13.907	27.558	-1.956	1.00 33.04
ATOM	1243		PHE A		13.402	27.404	-3.255	1.00 37.29
ATOM	1244	CD2		459	15.168	28.122	-1.789	1.00 32.57
ATOM	1245	CE1			14.142	27.809	-4.360	1.00 33.63
ATOM	1246	CE2		459	15.920	28.533	-2.886	1.00 36.16
ATOM	1247	CZ	PHE A		15.407	28.378	-4.175	1.00 37.49
	1247	C	PHE A		14.331	25.008	-0.495	1.00 28.01
MOTA	1249	Ö	PHE A		14.743	24.252	-1.372	1.00 29.21
ATOM	1250	N	VAL A		15.067	25.334	0.553	1.00 29.05
ATOM	1251	CA	VAL A		16.407	24.798	0.701	1.00 26.40
ATOM	1471	CA	VALU A	. 100				
			-					

WO 03/093312 PCT/EP03/04433

- 51 -

ATOM	1252	CB	VAL A	460	17.143	25.531	1.839	1.00 28.85
ATOM	1253	CG1	VAL A		18.470	24.967	2.044	1.00 34.54
	1254		VAL A		17.319	26.974	1.484	1.00 30.19
MOTA			VAL A		16.385	23.268	0.889	1.00 24.40
ATOM	1255	C			17.295	22.563	0.447	1.00 25.65
MOTA	1256	0	VAL A					1.00 24.80
MOTA	1257	N	LEU A	461	15.307	22.743	1.469	
ATOM	1258	CA	LEU A	461	15.194	21.297	1.700	1.00 26.95
ATOM	1259	CB	LEU A	461	14.034	21.015	2.653	1.00 28.61
ATOM	1260	CG	LEU A		14.024	19.600	3.228	1.00 30.23
			LEU A		15.049	19.523	4.335	1.00 30.35
MOTA	1261				12.637	19.257	3.751	1.00 37.76
MOTA	1262	_	LEU A			20.496	0.416	1.00 27.27
ATOM	1263	С	LEU A		14.966			
ATOM	1264	0	LEU A	461	15.566	19.430	0.198	1.00 26.82
ATOM	1265	N	MET A	462	14.023	20.991	-0.380	1.00 27.27
ATOM	1266	CA	MET A		13.650	20.378	-1.640	1.00 30.35
	1267	CB	MET A		12.196	20.707	-1.964	1.00 30.76
MOTA			MET A		11.213	20.255	-0.874	1.00 41.65
MOTA	1268	CG				18.462	-0.489	1.00 43.91
MOTA	1269	SD	MET A		11.153			1.00 47.33
MOTA	1270	CE	MET A		10.018	17.928	-1.767	
ATOM	1271	С	MET A	462	14.574	20.870	-2.730	1.00 29.93
MOTA	1272	0	MET A	462	14.135	21.418	-3.729	1.00 33.71
ATOM	1273	N	SER A		15.864	20.657	-2.524	1.00 30.81
		CA	SER A		16.881	21.064	-3.470	1.00 35.27
MOTA	1274				18.143	21.489	-2.730	1.00 36.89
MOTA	1275	CB	SER A				-3.578	1.00 50.70
MOTA	1276	OG	SER A		18.963	22.273		1.00 36.64
ATOM	1277	С	SER A		17.174	19.889	-4.411	
MOTA	1278	0	SER A	463	17.599	18.819	-3.976	1.00 32.89
ATOM	1279	N	ALA A	464	16.925	20.096	-5.702	1.00 39.89
ATOM	1280	CA	ALA A		17.127	19.053	-6.698	1.00 40.73
	1281	CB	ALA A		16.425	19.425	-7.980	1.00 39.42
MOTA					18.585	18.728	-6.969	1.00 42.63
ATOM	1282	Ç	ALA A				-7.401	1.00 48.91
MOTA	1283	0	ALA A		18.897	17.616		1.00 43.62
MOTA	1284	N	ASP A	465	19.481	19.663	-6.656	1.00 43.62
ATOM	1285	CA	ASP A	465	20.905	19.461	-6.908	1.00 43.08
ĀTŪM	1286	CB	ASP A	465	21.546	20.754	-7.398	1.00 49.21
MOTA	1287	CG	ASP A		21.620	21.805	-6.324	1.00 54.48
	1288	OD1			22.753	22.243	-6.029	1.00 56.04
MOTA					20.555	22.184	-5.783	1.00 57.56
MOTA	1289	OD2			21.766	18.855	-5.803	1.00 41.94
MOTA	1290	С	ASP A				-5.677	1.00 46.76
MOTA	1291	0	ASP A		22.946	19.191		
MOTA	1292	N	ARG A	466	21.190	17.995	-4.976	1.00 37.97
ATOM	1293	CA	ARG A	466	21.987	17.342	-3.953	1.00 34.33
ATOM	1294	CB	ARG A	466	21.112	16.818	-2.804	1.00 31.22
ATOM	1295	CG	ARG A		20.380	17.869	-2.006	1.00 27.68
	1296	CD	ARG A		21.340	18.803	-1.302	1.00 27.64
MOTA			ARG A		20.588	19.665	-0.400	1.00 26.47
ATOM	1297	NE			21.076	20.728	0.234	1.00 24.01
MOTA	1298	CZ	ARG A				0.092	1.00 20.35
MOTA	1299	NH1	ARG A	466	22.341	21.082		1.00 25.10
MOTA	1300	NH2	ARG A	466	20.266	21.477	0.969	1.00 25.10
MOTA	1301	C	ARG A	466	22.613	16.155	-4.681	1.00 32.20
ATOM	1302	0	ARG A	466	21.981	15.542	-5.543	1.00 34.80
ATOM	1303	N	SER A		23.852	15.835	-4.343	1.00 31.72
		CA	SER A		24.512	14.700	-4.961	1.00 29.23
ATOM	1304				25.915	14.497	-4.373	1.00 30.36
MOTA	1305	CB	SER A			15.613	-4.579	1.00 34.62
ATOM	1306	OG	SER A		26.750			
ATOM	1307	С	SER A	467	23.705	13.442	-4.680	1.00 29.79
MOTA	1308	0	SER A	467	23.050	13.327	-3.653	1.00 27.96
ATOM	1309	N	TRP A		23.760	12.504	-5.610	1.00 27.51
ATOM	1310	CA	TRP A		23.114	11.203	-5.476	1.00 27.13
ATOM	1311	CB	TRP A		23.703	10.431	-4.286	1.00 30.38
			TRP A		25.196	10.650	-4.109	1.00 33.34
ATOM	1312	CG				10.375	-5.068	1.00 34.52
ATOM	1313	CD2			26.241			1.00 34.97
MOTA	1314	CE2			27.453	10.853	-4.510	
MOTA	1315	CE3			26.271	9.778	-6.345	1.00 33.99
ATOM	1316	CD1	L TRP A	468	25.807	11.246	-3.043	1.00 35.05
ATOM	1317		L TRP A		27.152	11.376	-3.278	1.00 35.95

MOM	1318	C72	TRP A 46	R	28.688	10.755	-5.182	1.00	32.97
MOTA	1319		TRP A 46		27.494	9.677	-7.012	1.00	29.70
ATOM			TRP A 46		28.686	10.167	-6.425		34.34
ATOM	1320				21.602	11.121	-5.472		27.07
MOTA	1321		TRP A 46		21.042	10.084	-5.105		29.52
MOTA	1322		TRP A 46				-5.874		27.42
ATOM	1323		LEU A 46		20.921	12.190			
MOTA	1324		LEU A 46		19.456	12.139	-5.945		30.07
ATOM	1325	CB	LEU A 46	9	18.910	13.539	-6.099		28.28
ATOM	1326	CG	LEU A 46	9	18.898	14.353	-4.824		24.65
ATOM	1327	CD1	LEU A 46	9	18.463	.15.758	-5.160		26.09
ATOM	1328		LEU A 46		17.929	13.704	-3.867	1.00	20.08
ATOM	1329	C	LEU A 46	9	19.028	11.294	-7.155	1.00	33.83
ATOM	1330		LEU A 46		19.735	11.285	-8.146	1.00	39.39
	1331	Ŋ	GLN A 47		17.916	10.564	-7.077	1.00	34.69
MOTA	1332	CA	GLN A 47		17.463	9.757	-8.224	1.00	39.38
ATOM		CB	GLN A 47		16.832	8.443	-7.779	1.00	40.10
ATOM	1333		GLN A 47		17.796	7.485	-7.120		50.51
ATOM	1334	CG			17.111	6.245	-6.571		55.73
MOTA	1335	CD	GLN A 47		15.993	5.911	-6.964		57.73
MOTA	1336	-	GLN A 47			5.565	-5.643		58.82
MOTA	1337	NE2	GLN A 47		17.776		-9.050		40.91
MOTA	1338	С	GLN A 47		16.444	10.524			42.98
MOTA	1339	0	GLN A 47		16.619	10.727	-10.250		
MOTA	1340	N	GLU A 47		15.383	10.960	-8.386		40.83
MOTA	1341	CA	GLU A 47		14.308	11.720	-9.013		40.88
ATOM	1342	CB	GLU A 47	1	13.001	11.447	-8.269		40.93
ATOM	1343	CG	GLU A 47	1	12.699	9.972	-8.077		48.61
ATOM	1344	CD	GLU A 47		11.560	9.737	-7.098		53.74
ATOM	1345	OE1	GLU A 47	1	10.392	10.051	-7.438		52.66
ATOM	1346	OE2	GLU A 47		11.841	9.243	-5.981		59.20
ATOM	1347	C	GLU A 47		14.588	13.235	-9.046		41.53
ATOM	1348	Ō	GLU A 47		13.780	14.027	-8.551		42.72
ATOM	1349	Ň	LYS A 47		15.707	13.634	-9.657	1.00	41.50
ATOM	1350	CA	LYS A 47		16.086	15.044	-9.750	1.00	41.09
ATOM	1351	CB	LYS A 47		17.332		-10.614	1.00	38.72
	1352	CG	LYS A 47	2	18.592	14.669	-9.971	1.00	43.30
ATOM		CD	LYS A 47		19.731	15.695	-10.033		46.29
ATOM	1353		LYS A 47		20.679	15.517	-8.831	1.00	
ATOM	1354	CE	LYS A 47		21.892	16.398	-8.804		46.13
ATOM	1355	NZ	LYS A 47		14.978		-10.287	1.00	
MOTA	1356	C	LYS A 47		14.628	16.963	-9.689		43.75
ATOM	1357	0			14.399		-11.402	1.00	
MOTA	1358	N	VAL A 47		13.326		-12.084	1.00	
ATOM	1359	CA	VAL A 47		12.963		-13.416		49.53
ATOM	1360	CB	VAL A 47		11.696		-14.040	1.00	
ATOM	1361	CG1	VAL A 47		14.155		-14.395		49.56
ATOM	1362	CG2	VAL A 47				-11.235		37.01
ATOM	1363	C	VAL A 47		12.076		-11.212		33.80
MOTA	1364	0	VAL A 47	/ 3	11.536		-10.570		36.39
MOTA	1365	N	LYS A 47		11.609	15.415		1.00	36.93
ATOM	1366	CA	LYS A 47		10.440	15.508	-9.695		
ATOM	1367	CB	LYS A 47	74	10.084	14.126	-9.147		35.35
ATOM	1368	CG	LYS A 47		8.886	14.077	-8.218	1.00	38.41
ATOM	1369	CD	LYS A 47	74	8.579	12.626	-7.848		46.48
ATOM	1370	CE	LYS A 47		7.746	12.480	-6.569		53.40
ATOM	1371	NZ	LYS A 47	74	6.298	12.790	-6.709		57.86
ATOM	1372	С	LYS A 47	74	10.713	16.495	-8.537		37.36
ATOM	1373	0	LYS A 47		9.887	17.359	-8.250		36.85
ATOM	1374	N	ILE A 4	75	11.897	16.422	-7.927		37.31
MOTA	1375	CA	ILE A 4		12.231	17.328	-6.820		37.61
ATOM	1376	CB	ILE A 4		13.535	16.887	-6.067	1.00	35.04
ATOM	1377	CG2			13.834	17.877	-4.931	1.00	34.59
MOTA	1378	CG1	ILE A 4		13.368	15.464	-5.488	1.00	27.42
ATOM	1379	CD1		75	14.680	14.711	-5.243	1.00	18.44
ATOM	1380	C	ILE A 4		12.349	18.766	-7.352		40.05
ATOM	1381	ŏ	ILE A 4		11.882	19.727	-6.721	1.00	38.84
ATOM	1382	N	GLU A 4	76	12.913	18.896	-8.550	1.00	41.69
	1383	CA	GLU A 4	76	13.066	20.184	-9.207		43.30
ATOM	7303	CA	JEU M 4					_	

7 COM	1384	CB GLU A 476	13.755	19.984	-10.552	1.00 48.95
ATOM			13.732	21.196		1.00 62.73
MOTA	1385					1.00 70.08
ATOM	1386	CD GLU A 476	14.355		-10.846	
ATOM	1387	OE1 GLU A 476	15.464		-10.274	1.00 76.26
ATOM	1388	OE2 GLU A 476	13.741	23.532	-10.947	1.00 75.60
			11.705	20.850	-9.413	1.00 42.70
ATOM	1389				-	1.00 38.37
MOTA	1390	O GLU A 476	11.547	22.050	-9.183	
ATOM	1391	N LYS A 477	10.724	20.066	-9.854	1.00 41.95
ATOM	1392	CA LYS A 477	9.379	20.580	-10.072	1.00 45.24
			8.461		-10.643	1.00 49.85
MOTA	1393				-11.905	1.00 59.55
MOTA	1394	CG LYS A 477	8.971			
MOTA	1395	CD LYS A 477	9.158		-12.984	1.00 69.14
ATOM	1396	CE LYS A 477	9.721	19.258	-14.243	1.00 75.50
	1397	NZ LYS A 477	9.631	20.220	-15.382	1.00 82.60
ATOM			8.798	21.075	-8.753	1.00 45.20
ATOM	1398	C LYS A 477				1.00 44.88
ATOM	1399	O LYS A 477	8.303	22.207	-8.668	
MOTA	1400	N LEU A 478	8.850	20.216	-7.728	1.00 42.02
ATOM	1401	CA LEU A 478	8.339	20.575	-6.403	1.00 39.03
	1402	CB LEU A 478	8.506	19.411	-5.419	1.00 38.50
ATOM			7.562	18.213	-5.609	1.00 38.77
ATOM	1403	CG LEU A 478				1.00 40.42
ATOM	1404	CD1 LEU A 478	7.919	17.062	-4.658	
ATOM	1405	CD2 LEU A 478	6.126	18.653	-5.389	1.00 36.80
ATOM	1406	C LEU A 478	9.020	21.856	-5.875	1.00 37.92
			8.332	22.767	-5.399	1.00 37.49
ATOM	1407		10.344	21.963	-6.057	1.00 37.80
ATOM	1408	N GLN A 479				1.00 38.11
ATOM	1409	CA GLN A 479	11.083	23.144	-5.607	
ATOM	1410	CB GLN A 479	12.610	22.987	-5.772	1.00 36.91
ATOM	1411	CG GLN A 479	13.425	24.177	-5.189	1.00 40.17
		CD GLN A 479	14.938	24.122	-5.452	1.00 42.02
ATOM	1412		15.411	23.469	-6.392	1.00 48.01
MOTA	1413	OE1 GLN A 479				1.00 46.19
MOTA	1414	NE2 GLN A 479	15.702	24.820	-4.616	
MOTA	1415	C GLN A 479	10.589	24.379	-6.343	1.00 39.25
ATOM	1416	O GLN A 479	10.392	25.426	-5.718	1.00 42.08
	1417		10.348	24.251	-7.650	1.00 39.34
ATOM			9.855	25.371	-8.460	1.00 43.07
ATOM	1418	CA GLN A 480				1.00 51.07
MOTA	1419	CB GLN A 480	9.547	24.917	-9.894	
ATOM	1420	CG GLN A 480	10.733		-10.707	1.00 64.44
ATOM	1421	CD GLN A 480	10.291		-11.889	1.00 73.00
ATOM	1422	OE1 GLN A 480	9.132	23.582	-12.310	1.00 75.34
			11.211		-12.425	1.00 72.93
ATOM	1423			25.987	-7.853	1.00 37.24
ATOM	1424	C GLN A 480	8.591			
ATOM	1425	O GLN A 480	8.499	27.198	-7.658	1.00 35.48
ATOM	1426	N LYS A 481	7.620	25.139	-7.545	1.00 35.17
ATOM	1427	CA LYS A 481	6.381	25.614	-6.957	1.00 37.36
	1428	CB LYS A 481	5.397	24.470	-6.801	1.00 41.26
ATOM			4.877	23.975	-8.112	1.00 49.18
ATOM	1429	CG LYS A 481				1.00 59.24
ATOM	1430	CD LYS A 481	3.683	23.105	-7.907	
MOTA	1431	CE LYS A 481	2.989	22.839	-9.229	1.00 68.40
ATOM	1432	NZ LYS A 481	1.798	21.950	-9.050	1.00 76.15
MOTA	1433	C LYS A 481	6.599	26.317	-5.628	1.00 37.73
		404	5.976	27.353	-5.360	1.00 35.72
MOTA	1434		7.486	25.748	-4.806	1.00 38.76
MOTA	1435	N ILE A 482				
MOTA	1436	CA ILE A 482	7.831	26.299	-3.494	
MOTA	1437	CB ILE A 482	8.817	25.381	-2.705	1.00 32.89
ATOM	1438	CG2 ILE A 482		26.130	-1.514	1.00 34.55
		CG1 ILE A 482		24.093	-2.234	1.00 28.40
ATOM	1439			23.005	-1.769	1.00 24.86
ATOM	1440	CD1 ILE A 482				1.00 35.37
MOTA	1441	C ILE A 482	8.447	27.681	-3.639	
MOTA	1442	O ILE A 482	8.152	28.579	-2.864	1.00 36.18
ATOM	1443	N GLN A 483		27.862	-4.668	1.00 38.47
MOTA	1444	CA GLN A 483		29.164	-4.892	1.00 39.76
				29.071	-5.950	1.00 40.59
MOTA	1445			30.342	-6.053	1.00 49.20
ATOM	1446	CG GLN A 483				
MOTA	1447	CD GLN A 483		30.296	-7.192	1.00 58.50
ATOM	1448	OE1 GLN A 483	12.820	29.303	-7.861	1.00 65.68
ATOM	1449	NE2 GLN A 483	13.440	31.368	-7.409	1.00 65.23
						•

ATOM 1450 C GLN A 483							20.020	E 204	1 00 40	0.4
ATOM 1452 N 1484 1452 N 1484 6.754 30.730 -6.439 1.00 42.15 1ATOM 1453 CA 1484 6.754 30.730 -6.439 1.00 42.15 1ATOM 1454 CB 1455 CG 1481 484 6.754 30.730 -6.439 -6.46 1ATOM 1455 CG 1457 CD2_1481 484 6.937 20.033 -7.416 1.00 45.74 1ATOM 1455 CG 1457 CD2_1481 484 6.937 20.033 -7.416 1.00 48.20 1ATOM 1457 CD2_1481 484 6.966 30.856 -9.472 1.00 50.25 1ATOM 1458 C 1459 O 1461 CA 1463 C 1461 CA 1463 C 1461 CA 1464 C 1464 CA 1464 C 1465 CA 1465 CA 1465 CA 1466 CA 1467 CB 1467 CB 1468 CG 1468 CG 1468 CG 1468 CG 1468 CG 1468 CG 1469 CD1 1467 CB 1468 CG 1	MOTA	1450	С							
ATOM 1452 N LEU A 484	ATOM	1451	0	GLN A	483	8.969				
ATOM 1454 CB LEU A 484			N	LEU A	484	7.802	29.820	-6.002		
ATOM 1455 CB LEU A 484 6,403 29,624 -8,765 1,00 45,74						6.754	30.730	-6.439	1.00 42	2.14
ATOM 1455 CG LEU A 484								-7.416	1.00 45	5.74
ATOM 1456 CDI LEU A 484 5.337 28.943 -9.615 1.00 48.20 ATOM 1457 CD2 LEU A 484 6.666 30.856 -9.615 1.00 42.55 ATOM 1458 C LEU A 484 5.957 31.241 -5.252 1.00 42.55 ATOM 1459 C LEU A 484 5.957 31.241 -5.252 1.00 42.55 ATOM 1469 N ALA A 485 5.626 30.329 -4.338 1.00 43.56 ATOM 1461 CA ALA A 485 4.872 30.672 -3.138 1.00 43.56 ATOM 1462 CB ALA A 485 4.872 30.672 -3.138 1.00 40.84 ATOM 1463 C ALA A 485 5.729 31.497 -2.2449 1.00 41.40 ATOM 1463 C ALA A 485 5.729 31.497 -2.2451 1.00 37.52 ATOM 1464 O ALA A 485 5.204 12.298 -1.388 1.00 37.52 ATOM 1465 N LEU A 486 7.979 32.036 -1.380 1.00 37.52 ATOM 1466 CA EUU A 486 7.979 32.036 -1.380 1.00 38.02 ATOM 1467 CB LEU A 486 9.371 31.401 -1.389 1.00 32.53 ATOM 1468 CG LEU A 486 10.451 32.287 -0.758 1.00 33.217 ATOM 1470 CD2 LEU A 486 11.818 31.693 -0.965 1.00 33.217 ATOM 1471 C LEU A 486 8.007 34.446 -1.190 1.00 44.54 ATOM 1471 C LEU A 486 8.007 34.446 -1.190 1.00 44.54 ATOM 1472 O LEU A 486 8.007 34.446 -1.190 1.00 44.54 ATOM 1474 CA GLN A 487 8.007 33.454 -3.271 1.00 44.54 ATOM 1475 CB GLN A 487 8.007 33.454 -3.271 1.00 44.56 ATOM 1476 CG GLN A 487 8.007 33.545 -3.271 1.00 44.56 ATOM 1476 CG GLN A 487 9.000 35.408 -6.310 1.00 61.53 ATOM 1477 CD GLN A 487 9.008 33.587 -7.865 1.00 31.01 61.53 ATOM 1478 OEL GLN A 487 9.000 35.408 -6.310 1.00 61.53 ATOM 1478 OEL GLN A 487 9.003 33.587 -7.865 1.00 47.16 ATOM 1478 OEL GLN A 487 9.003 33.587 -7.865 1.00 47.16 ATOM 1479 NE2 GLN A 487 9.003 33.587 -7.865 1.00 47.16 ATOM 1479 NE2 GLN A 487 9.003 33.587 -7.865 1.00 47.16 ATOM 1479 NE2 GLN A 487 9.003 33.587 -7.865 1.00 47.06 6.75 ATOM 1480 C GLN A 487 9.003 33.587 -7.865 1.00 47.06 6.75 ATOM 1481 0 GLN A 487 9.003 33.587 -7.865 1.00 47.06 6.75 ATOM 1481 0 GLN A 487 9.003 33.587 -7.865 1.00 47.06 6.75 ATOM 1481 0 GLN A 487 9.003 33.587 -7.865 1.00 47.06 6.75 ATOM 1481 0 GLN A 487 9.003 33.587 -7.865 1.00 47.06 6.75 ATOM 1481 0 GLN A 488 9.007 33.38 33.587 -7.865 1.00 47.06 6.75 ATOM 1481 0 GLN A 488 9.007 33.38 33.587 -7.865 1.00 47.06 6.75 ATOM 1481 0 GLN A 488 9.007 33.38 33.587 -7.86			_							
ATOM 1457 CD2 LEU A 484										
ATOM 1459 O LEU A 484 5.957 31.241 -5.252 1.00 42.55 ATOM 1459 O LEU A 484 5.622 32.424 -5.181 1.00 42.64 ATOM 1461 CA ALA A 485 5.626 30.329 -4.338 1.00 43.56 ATOM 1461 CA ALA A 485 4.872 30.672 -3.138 1.00 43.56 ATOM 1462 CB ALA A 485 4.872 30.672 -3.138 1.00 43.56 ATOM 1462 CB ALA A 485 4.872 30.672 -3.138 1.00 43.56 ATOM 1463 C ALA A 485 5.626 30.329 -4.338 1.00 37.33 ATOM 1464 O ALA A 485 5.729 31.497 -2.162 1.00 37.33 ATOM 1465 N LEU A 486 7.047 31.293 -2.215 1.00 35.33 ATOM 1466 CA LEU A 486 7.047 31.293 -2.215 1.00 35.33 ATOM 1466 CA LEU A 486 7.047 31.293 -2.215 1.00 35.33 ATOM 1467 CB LEU A 486 10.451 32.287 -0.758 1.00 33.25 ATOM 1469 CDI LEU A 486 10.451 32.287 -0.758 1.00 33.21 ATOM 1470 CDZ LEU A 486 10.176 32.478 0.723 1.00 33.21 ATOM 1471 C LEU A 486 8.049 33.457 -1.942 1.00 44.35 ATOM 1472 O LEU A 486 8.049 33.457 -1.942 1.00 44.35 ATOM 1473 N GLN A 487 8.102 33.545 -3.271 1.00 44.53 ATOM 1474 CA CLEU A 486 8.049 33.457 -1.942 1.00 44.35 ATOM 1474 CA CLEU A 486 8.049 33.457 -1.942 1.00 44.54 ATOM 1474 CA CLEU A 486 8.049 33.457 -1.942 1.00 44.55 ATOM 1474 CA CLEU A 486 8.049 33.457 -1.942 1.00 44.55 ATOM 1474 CA CLEU A 486 8.049 33.457 -1.942 1.00 44.55 ATOM 1474 CA CLEU A 486 8.049 33.457 -1.942 1.00 44.55 ATOM 1474 CA CLEU A 486 8.077 34.481 -1.10 1.00 44.55 ATOM 1474 CA CLEU A 486 8.049 33.457 -1.942 1.00 44.55 ATOM 1474 CA CLEU A 486 8.049 33.457 -1.942 1.00 44.55 ATOM 1474 CA CLEU A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1474 CA CLEU A 487 8.103 ATOM 1475 CB GLN A 487 8.145 34.502 -5.486 1.00 51.86 ATOM 1476 CG GLN A 487 8.145 34.502 -5.486 1.00 51.86 ATOM 1476 CG GLN A 487 9.083 33.555 -3.271 1.00 44.64 ATOM 1478 OEI GLN A 487 9.083 33.557 -7.655 1.00 66.76 ATOM 1480 C GLN A 487 9.083 33.557 -7.555 1.00 66.76 ATOM 1480 C GLN A 487 9.083 33.557 -7.555 1.00 66.76 ATOM 1480 C GLN A 488 9.070 35.373 -8.311 1.00 47.07 ATOM 1480 C GLN A 488 488 1.638 33.939 -1.7555 1.00 65.56 ATOM 1480 C GLN A 488 488 1.638 33.939 -1.7555 1.00 65.65 ATOM 1480 C C GLN A 488 488 1.638 33.939 -1.7555 1.00 65.65 A	ATOM		CD1	LEU A	484					
ATOM 1460 N ALA 484 5 .622 32.424 -5.181 1.00 42.64 ATOM 1461 CA ALA 485 5.622 30.329 -4.338 1.00 43.56 ATOM 1461 CA ALA 485 5.623 30.329 -4.338 1.00 40.84 ATOM 1462 CB ALA 485 4.350 29.403 -2.449 1.00 41.40 ATOM 1463 C ALA 485 5.729 31.497 -2.162 1.00 37.33 ATOM 1464 O ALA 485 5.729 31.497 -2.162 1.00 37.33 ATOM 1465 N LEU A 486 7.047 31.293 -2.215 1.00 37.33 ATOM 1466 CA LEU A 486 7.979 32.036 -1.380 1.00 38.02 ATOM 1467 CB LEU A 486 9.371 31.401 -1.395 1.00 32.53 ATOM 1468 CG LEU A 486 10.451 32.287 -0.758 1.00 33.251 ATOM 1469 CD1 LEU A 486 10.451 32.287 -0.758 1.00 33.21 ATOM 1470 CD2 LEU A 486 11.818 31.693 -0.965 1.00 31.01 ATOM 1471 C LEU A 486 8.049 33.457 -1.942 1.00 42.86 ATOM 1472 O LEU A 486 8.077 34.446 -1.190 1.00 44.54 ATOM 1473 N GLN A 487 8.070 33.545 -3.271 1.00 44.54 ATOM 1474 CA GLN A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1476 CG GLN A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1477 CD GLN A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1478 OEI GLN A 487 9.000 35.408 -6.310 1.00 61.53 ATOM 1478 OEI GLN A 487 9.083 33.587 -7.865 1.00 65.86 ATOM 1479 NE2 GLN A 487 9.083 33.587 -7.865 1.00 61.53 ATOM 1480 C GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1480 C GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1481 O GLN A 487 6.844 36.754 -3.307 1.00 45.157 ATOM 1480 C GLN A 487 9.083 33.587 -7.865 1.00 67.66 ATOM 1481 O GLN A 487 6.844 36.754 -3.307 1.00 45.157 ATOM 1481 O GLN A 488 3.925 37.997 -1.655 1.00 47.05 ATOM 1480 C GLN A 488 3.925 37.997 -1.757 1.00 66.76 ATOM 1481 O GLN A 488 3.925 37.997 -1.757 1.00 66.76 ATOM 1482 N HIS A 488 4.387 35.405 -3.422 1.00 48.67 ATOM 1480 C GLN A 488 5.095 34.844 -1.500 1.00 65.57 ATOM 1480 C GLN A 488 5.500 37.70 35.17 1.00 48.67 ATOM 1480 C GLN A 488 5.500 37.70 35.17 1.00 48.67 ATOM 1480 C GLN A 488 5.500 37.70 35.17 1.00 48.67 ATOM 1490 C GLN A 488 5.500 37.70 35.17 1.00 48.67 ATOM 1491 O HIS A 488 1.097 35.37 3.831 1.00 40	ATOM	1457	CD2							
ATOM 1459 O LEU A 484 5.622 32.424 -5.181 1.00 42.56 ATOM 1461 CA ALA A 485 6.626 30.329 -4.338 1.00 43.56 ATOM 1461 CA ALA A 485 4.872 30.672 -3.128 1.00 40.84 ATOM 1462 CB ALA A 485 5.729 31.497 -2.162 1.00 37.33 ATOM 1464 O ALA A 485 5.729 31.497 -2.162 1.00 37.33 ATOM 1465 N LEU A 486 7.047 31.293 -2.215 1.00 33.53 ATOM 1466 CA LEU A 486 7.047 31.293 -2.215 1.00 33.53 ATOM 1466 CA LEU A 486 9.371 31.401 -1.395 1.00 38.02 ATOM 1467 CB LEU A 486 9.371 31.401 -1.395 1.00 32.53 ATOM 1468 CG LEU A 486 10.451 32.287 -0.758 1.00 33.23 ATOM 1469 CDL LEU A 486 10.451 32.287 -0.758 1.00 33.27 ATOM 1470 CD2 LEU A 486 8.049 33.457 -1.942 1.00 42.86 ATOM 1471 C LEU A 486 8.049 33.457 -1.942 1.00 42.86 ATOM 1472 O LEU A 486 8.049 33.457 -1.942 1.00 42.86 ATOM 1473 N GLN A 487 8.070 33.545 -3.271 1.00 44.54 ATOM 1474 CA GLN A 487 8.070 33.545 -3.271 1.00 44.54 ATOM 1475 CB GLN A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1475 CB GLN A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1476 CG GLN A 487 9.000 35.408 -6.310 1.00 61.58 ATOM 1479 NEZ GLN A 487 9.083 33.587 -7.865 1.00 65.93 ATOM 1479 NEZ GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1470 CB GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1470 CB GLN A 487 9.083 33.587 -7.865 1.00 47.16 ATOM 1478 OEI GLN A 487 9.083 33.587 -7.865 1.00 47.16 ATOM 1478 OEI GLN A 487 9.083 33.587 -7.865 1.00 47.16 ATOM 1478 OEI GLN A 487 9.083 33.587 -7.865 1.00 47.16 ATOM 1480 CB GLN A 487 9.083 33.587 -7.865 1.00 47.16 ATOM 1481 O GLN A 487 9.083 33.587 -7.865 1.00 47.06 ATOM 1480 CB GLN A 488 9.083 33.587 -7.865 1.00 47.06 ATOM 1481 O GLN A 487 9.083 33.587 -7.865 1.00 47.06 ATOM 1481 O GLN A 488 8.007 34.874 4.3741 1.00 47.07 60 ATOM 1481 O GLN A 488 8.007 34.874 4.3741 1.00 47.07 60 ATOM 1481 O GLN A 488 8.007 34.874 4.3741 1.00 47.07 60 ATOM 1481 O GLN A 488 8.007 35 34.874 -3.741 1.00 47.07 60 ATOM 1480 CB GLN A 488 8.007 37 34.340 -3.423 1.00 48.67 ATOM 1480 CB GLN A 488 8.007 37 34.340 -3.3423 1.00 48.67 ATOM 1480 CB GLN A 488 8.007 37 34.340 -3.3423 1.00 48.67 ATOM 1480 CB GLN A 488 9.	MOTA	1458	С	LEU A	484	5.957	31.241			
ATOM 1461 CA ALA				LEU A	484	5.622	32.424	-5.181	1.0042	2.64
ATOM 1461 CA ALA 485						5.626	30.329	-4.338	1.00 43	3.56
ATOM 1463 C B ALA A 485								-3.128	1.00 40).84
ATOM 1463										
ATOM 1465 N LEU A 486 7.047 31.293 -2.215 1.00 35.33 ATOM 1465 N LEU A 486 7.979 32.036 -1.380 1.00 35.33 ATOM 1466 CA LEU A 486 9.371 31.401 -1.395 1.00 35.33 ATOM 1467 CB LEU A 486 10.451 32.287 -0.758 1.00 33.21 ATOM 1468 CG LEU A 486 10.176 32.478 0.723 1.00 33.21 ATOM 1469 CD1 LEU A 486 10.176 32.478 0.723 1.00 33.21 ATOM 1470 CD2 LEU A 486 10.176 32.478 0.723 1.00 32.21 ATOM 1470 CD2 LEU A 486 8.049 33.457 -1.942 1.00 42.86 ATOM 1470 CD2 LEU A 486 8.049 33.457 -1.942 1.00 42.86 ATOM 1472 O LEU A 486 8.049 33.457 -1.942 1.00 44.35 ATOM 1472 O LEU A 486 8.077 34.446 -1.190 1.00 44.35 ATOM 1473 N GLN A 487 8.12 34.481 3-3.998 1.00 47.16 ATOM 1474 CA GLN A 487 8.12 34.813 -3.998 1.00 47.16 ATOM 1476 CG GLN A 487 8.12 34.502 -5.486 1.00 51.53 ATOM 1476 CG GLN A 487 9.000 35.408 -6.310 1.00 61.53 ATOM 1478 OE1 GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1478 OE1 GLN A 487 9.083 33.587 -7.865 1.00 65.76 ATOM 1478 OE1 GLN A 487 9.083 33.587 -7.865 1.00 65.76 ATOM 1480 C GLN A 487 6.823 35.579 -3.655 1.00 47.06 ATOM 1481 O GLN A 487 6.823 35.579 -3.655 1.00 47.07 ATOM 1481 O GLN A 487 6.823 35.579 -3.655 1.00 47.07 ATOM 1482 N HIS A 488 5.702 34.874 -3.741 1.00 45.17 ATOM 1483 CA HIS A 488 5.702 34.874 -3.741 1.00 47.07 ATOM 1483 CA HIS A 488 5.702 34.874 -3.741 1.00 47.07 ATOM 1486 CD LHS A 488 1.638 33.939 -1.715 1.00 66.96 ATOM 1488 CBI HIS A 488 1.638 33.939 -1.715 1.00 66.91 ATOM 1488 CBI HIS A 488 1.638 33.939 -1.715 1.00 66.91 ATOM 1489 CD HIS A 488 1.638 33.939 -1.715 1.00 66.91 ATOM 1489 CD HIS A 488 1.638 33.939 -1.715 1.00 64.94 ATOM 1490 C HIS A 488 1.638 33.939 -1.715 1.00 64.94 ATOM 1490 C HIS A 488 1.638 33.939 -1.715 1.00 64.94 ATOM 1490 C HIS A 488 1.638 33.939 -1.715 1.00 64.94 ATOM 1490 C HIS A 488 1.638 33.939 -1.715 1.00 64.94 ATOM 1490 C HIS A 488 1.638 3.925 37.097 -1.757 1.00 48.67 ATOM 1490 C HIS A 488 1.638 3.925 37.097 -1.757 1.00 48.67 ATOM 1490 C C LEU A 490 7.865 37.097 -1.757 1.00 48.67 ATOM 1490 C C LEU A 490 7.865 37.097 -1.757 1.00 48.67 ATOM 1490 C C LEU A 490 7.865 37.097 -1.7										
ATOM 1465 N LEU A 486 7.047 31.293 -2.215 1.00 35.33 ATOM 1466 CA LEU A 486 7.979 32.036 -1.380 1.00 38.02 ATOM 1467 CB LEU A 486 9.371 31.401 -1.395 1.00 32.53 ATOM 1469 CD1 LEU A 486 10.451 32.287 -0.758 1.00 33.21 ATOM 1469 CD1 LEU A 486 10.176 32.478 0.723 1.00 32.27 ATOM 1470 CD2 LEU A 486 11.818 31.693 -0.965 1.00 31.01 ATOM 1471 C LEU A 486 8.049 33.457 -1.942 1.00 42.86 ATOM 1473 N GLN A 487 8.103 3.491 -1.942 1.00 44.35 ATOM 1474 CA GLN A 487 8.112 34.813 -3.998 1.00 44.35 ATOM 1475 CB GLN A 487 8.145 34.502 -5.486 1.00 51.86 ATOM 1476 CG GLN A 487 8.145 34.502 -5.486 1.00 51.86 ATOM 1477 CD GLN A 487 9.000 35.408 -0.965 1.00 61.53 ATOM 1478 OEI GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1478 OEI GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1480 C GLN A 487 9.083 35.579 -3.655 1.00 47.06 ATOM 1480 C GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1480 C GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1482 N HIS A 488 4.387 35.405 -3.423 1.00 47.07 ATOM 1483 CA HIS A 488 4.387 35.405 -3.423 1.00 47.07 ATOM 1484 CB HIS A 488 4.387 35.405 -3.423 1.00 47.07 ATOM 1485 CG HIS A 488 4.387 35.405 -3.423 1.00 47.05 ATOM 1487 NDI HIS A 488 1.638 33.939 -1.715 1.00 65.76 ATOM 1488 CDHIS A 488 1.638 33.939 -1.715 1.00 65.76 ATOM 1489 NEZ HIS A 488 1.638 33.939 -1.715 1.00 65.51 ATOM 1489 NEZ HIS A 488 1.638 33.939 -1.715 1.00 65.61 ATOM 1490 C HIS A 488 1.638 33.939 -1.715 1.00 65.61 ATOM 1490 C HIS A 488 1.638 33.939 -1.715 1.00 65.61 ATOM 1490 C HIS A 488 1.638 33.939 -1.715 1.00 65.61 ATOM 1490 C HIS A 488 1.638 33.939 -1.715 1.00 65.61 ATOM 1490 C HIS A 488 1.638 33.939 -1.715 1.00 65.61 ATOM 1490 C HIS A 489 4.763 35.577 3.322 1.00 63.45 ATOM 1490 C HIS A 488 1.638 33.939 -1.715 1.00 65.61 ATOM 1490 C GLN A 489 4.763 35.770 3.0580 1.00 43.28 ATOM 1490 C GLO A 489 4.763 35.770 3.0580 1.00 43.28 ATOM 1490 C GLO A 489 4.763 35.770 3.0580 1.00 43.28 ATOM 1491 C VAL A 489 5.592 34.911 2.692 1.00 44.64 ATOM 1500 CG GLO A 490 7.224 4.00 37 0.498 1.00 50.68 ATOM 1500 CG GLO A 490 7.224 4.00 37 0.498 1.00 50.59 ATOM 1										
ATOM 1466 CB LEU A 486	ATOM	1464	0							
ATOM 1468 CG LEU A 486 10.451 32.287 -0.758 1.00 32.53 ATOM 1469 CD1 LEU A 486 10.176 32.478 -0.758 1.00 32.27 ATOM 1469 CD1 LEU A 486 10.176 32.478 -0.758 1.00 32.27 ATOM 1470 CD2 LEU A 486 11.818 31.693 -0.965 1.00 31.01 ATOM 1471 C LEU A 486 8.049 33.457 -1.942 1.00 42.86 ATOM 1471 C LEU A 486 8.077 34.446 -1.190 1.00 44.35 ATOM 1473 N GLN A 487 8.070 33.247 -1.942 1.00 44.56 ATOM 1473 N GLN A 487 8.070 33.545 -3.271 1.00 1.00 44.56 ATOM 1475 CB GLN A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1475 CB GLN A 487 9.003 35.408 -6.310 1.00 51.86 ATOM 1476 CG GLN A 487 9.003 35.408 -6.310 1.00 65.53 ATOM 1478 OEI GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1478 OEI GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1479 NE2 GLN A 487 9.083 33.557 -3.655 1.00 47.05 ATOM 1480 C GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1480 C GLN A 487 6.824 35.579 -3.655 1.00 47.05 ATOM 1481 O GLN A 488 6.823 35.579 -3.655 1.00 47.05 ATOM 1482 N HIS A 488 4.387 35.405 -3.423 1.00 47.07 ATOM 1482 N HIS A 488 4.387 35.405 -3.423 1.00 47.07 ATOM 1484 CB HIS A 488 4.387 35.405 -3.423 1.00 47.07 ATOM 1486 CD HIS A 488 4.387 35.405 -3.423 1.00 47.05 ATOM 1486 CD HIS A 488 4.387 35.405 -3.423 1.00 47.05 ATOM 1488 CD HIS A 488 1.638 33.939 -1.715 1.00 65.51 ATOM 1489 NE2 HIS A 488 1.638 33.939 -1.715 1.00 65.51 ATOM 1489 NE2 HIS A 488 1.638 33.939 -1.715 1.00 65.51 ATOM 1489 NE2 HIS A 488 1.638 33.939 -1.715 1.00 65.61 ATOM 1490 C HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1490 C HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1499 NE HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1499 NE LEU A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1490 C HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1490 C HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1490 C HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1499 NE LEU A 490 1.024 A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1490 C GL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1490 C GL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1490 C GL A 489 4.755 35.154 -1.00 41.10 65.61 ATOM 1500 CG LEU A 490 1.0389 36.884 -	ATOM	1465	N							
ATOM 1468 CG LEU A 486 9.371 31.401 -1.395 1.00 33.21 ATOM 1469 CD1 LEU A 486 10.451 32.287 -0.758 1.00 33.21 ATOM 1470 CD2 LEU A 486 10.176 32.478 0.723 1.00 33.21 ATOM 1471 C LEU A 486 11.818 31.693 -0.965 1.00 31.01 ATOM 1471 C LEU A 486 8.049 33.457 -1.942 1.00 42.86 ATOM 1472 O LEU A 486 8.077 34.446 -1.190 1.00 42.86 ATOM 1473 N GLN A 487 8.070 33.545 -3.271 1.00 44.64 ATOM 1473 N GLN A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1475 CB GLN A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1475 CB GLN A 487 9.000 35.408 -6.310 1.00 65.93 ATOM 1476 CG GLN A 487 9.000 35.408 -6.310 1.00 65.93 ATOM 1478 DEI GLN A 487 9.083 33.587 -7.865 1.00 65.93 ATOM 1478 DEI GLN A 487 9.083 33.587 -7.865 1.00 67.6 ATOM 1480 C GLN A 487 9.083 33.587 -7.865 1.00 47.05 ATOM 1481 O GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1481 O GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1482 N HIS A 488 4.387 6.844 36.754 -3.307 1.00 47.07 ATOM 1482 N HIS A 488 4.387 35.405 -3.423 1.00 47.05 ATOM 1485 CG HIS A 488 4.387 35.405 -3.423 1.00 47.05 ATOM 1486 CD2 HIS A 488 4.387 35.405 -3.423 1.00 47.05 ATOM 1486 CD2 HIS A 488 4.387 35.405 -3.423 1.00 48.67 ATOM 1486 CD2 HIS A 488 4.387 35.405 -3.423 1.00 49.05 ATOM 1488 CEI HIS A 488 1.097 35.377 -3.322 1.00 63.45 ATOM 1489 NE2 HIS A 488 1.097 35.371 -3.322 1.00 63.45 ATOM 1490 C HIS A 488 4.387 35.405 -3.423 1.00 49.05 ATOM 1490 C HIS A 488 4.387 35.571 -3.322 1.00 63.45 ATOM 1490 C HIS A 488 4.387 35.571 -3.322 1.00 63.45 ATOM 1490 C HIS A 488 4.383 35.962 -1.986 1.00 49.05 ATOM 1490 C HIS A 488 4.383 35.962 -1.986 1.00 49.05 ATOM 1490 C HIS A 488 4.383 35.962 -1.986 1.00 49.05 ATOM 1490 C HIS A 488 4.383 35.962 -1.986 1.00 49.05 ATOM 1490 C HIS A 488 4.383 35.962 -1.986 1.00 49.05 ATOM 1490 C HIS A 488 4.383 35.962 -1.986 1.00 49.05 ATOM 1490 C HIS A 488 4.383 35.962 -1.986 1.00 49.05 ATOM 1490 C HIS A 488 4.383 35.962 -1.986 1.00 49.05 ATOM 1490 C HIS A 488 4.383 35.962 -1.986 1.00 49.05 ATOM 1490 C WAL A 489 4.755 35.154 -1.021 1.00 48.47 ATOM 1490 C WAL A 489 4.755 35.154 -1.021 1.00 48.47 AT	ATOM	1466	CA	LEU A	486					
ATOM 1469 CD1 LEU A 486		1467	CB	LEU A	486	9.371	31.401	-1.395		
ATOM 1460 CD1 LEU A 486				LEU A	486	10.451	32.287	-0.758	1.00 33	3.21
ATOM 1470 CD2 LEU A 486						10.176		0.723	1.00 32	2.27
ATOM 1471 C LEU A 486 8.079 33.457 -1.942 1.00 42.86 ATOM 1472 O LEU A 486 8.077 34.446 -1.190 1.00 44.35 ATOM 1473 N GLN A 487 8.112 34.813 -3.271 1.00 44.64 ATOM 1475 CB GLN A 487 8.112 34.813 -3.271 1.00 44.64 ATOM 1475 CB GLN A 487 9.000 35.408 -6.310 1.00 61.53 ATOM 1476 CG GLN A 487 9.080 35.408 -6.310 1.00 65.93 ATOM 1477 CD GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1478 OE1 GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1479 NE2 GLN A 487 9.083 33.587 -7.865 1.00 67.06 ATOM 1480 C GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1481 O GLN A 487 6.824 36.754 -3.307 1.00 45.17 ATOM 1482 N HIS A 488 4.387 35.405 -3.271 1.00 45.17 ATOM 1483 CA HIS A 488 4.387 35.405 -3.231 1.00 48.67 ATOM 1485 CB HIS A 488 4.387 35.405 -3.233 1.00 48.67 ATOM 1486 C CD2 HIS A 488 4.387 35.405 -3.2368 1.00 59.15 ATOM 1486 CD2 HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1488 CE1 HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1488 CE1 HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.571 1.00 49.05 ATOM 1490 C HIS A 488 0.378 34.444 -1.571 1.00 49.05 ATOM 1491 O HIS A 488 0.378 34.444 -1.571 1.00 48.67 ATOM 1499 NE2 HIS A 488 0.378 34.444 -1.571 1.00 66.76 ATOM 1490 C HIS A 488 0.378 34.444 -1.571 1.00 64.94 ATOM 1491 O HIS A 488 0.378 34.444 -1.571 1.00 64.94 ATOM 1495 CGI VAL A 489 4.753 35.571 0.381 1.00 48.07 ATOM 1495 CGI VAL A 489 4.753 35.571 0.381 1.00 48.07 ATOM 1495 CGI VAL A 489 4.753 35.571 0.381 1.00 43.28 ATOM 1495 CGI VAL A 489 4.753 35.571 0.381 1.00 43.28 ATOM 1495 CGI VAL A 489 4.753 35.571 0.381 1.00 44.44 ATOM 1500 CG LEU A 490 7.865 37.761 0.101 1.100 54.00 ATOM 1503 CDI LEU A 490 7.385 37.763 0.103 1.00 45.44 ATOM 1500 CG LEU A 490 7.386 36.00 1.115 1.00 54.00 ATOM 1500 CG LEU A 490 7.338 39.122 -0.310 1.00 54.00 ATOM 1500 CG LEU A 490 7.338 39.922 -4.373 1.00 60.06 ATOM 1500 CG LEU A 490 7.338 39.922 -4.373 1.00 65.06 ATOM 1500 CG GLN A 491 6.560 4.523 -3.638 1.00 75.88 ATOM 1500 CG GLN A 491 6.560 4.523 -3.638 1.00 75.93 ATOM 1500 CG GLN A 491 6.560 4.524 4.0037 0.498 1.0								-0.965	1.00 33	L.01
ATOM 1472 O LEU A 486 8.077 34.446 -1.190 1.00 44.35 ATOM 1473 N GLN A 487 8.103 33.545 -3.271 1.00 44.64 ATOM 1474 CA GLN A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1475 CB GLN A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1475 CB GLN A 487 9.000 35.408 -6.310 1.00 61.53 ATOM 1477 CD GLN A 487 9.083 33.547 -7.865 1.00 66.76 ATOM 1479 NE2 GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1479 NE2 GLN A 487 9.083 33.587 -7.865 1.00 67.66 ATOM 1479 NE2 GLN A 487 9.083 35.579 -3.655 1.00 47.06 ATOM 1480 C GLN A 487 6.823 35.579 -3.655 1.00 47.07 ATOM 1481 O GLN A 487 6.823 35.579 -3.655 1.00 47.07 ATOM 1482 N HIS A 488 4.387 35.405 -33.423 1.00 48.67 ATOM 1482 N HIS A 488 4.387 35.405 -3.423 1.00 47.07 ATOM 1485 CG HIS A 488 4.387 35.405 -3.423 1.00 48.67 ATOM 1486 CD2 HIS A 488 2.095 34.484 -2.868 1.00 59.15 ATOM 1487 ND1 HIS A 488 1.037 35.317 -3.322 1.00 63.45 ATOM 1489 NE2 HIS A 488 1.097 35.317 -3.322 1.00 65.61 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1490 C HIS A 488 4.334 35.962 -1.986 1.00 49.05 ATOM 1491 O HIS A 488 4.334 35.962 -1.986 1.00 49.05 ATOM 1492 N VAL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1492 N VAL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1497 CC VAL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1497 CC VAL A 489 5.220 34.901 1.302 1.00 44.847 ATOM 1499 N LEU A 490 7.865 37.763 0.103 1.00 45.44 ATOM 1497 CC VAL A 489 5.220 34.901 1.302 1.00 44.84 ATOM 1499 N LEU A 490 7.865 37.763 0.103 1.00 49.05 ATOM 1500 CD LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1500 CD LEU A 490 7.865 37.765 0.100 1.100 54.10 ATOM 1500 CD LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1500 CD LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1500 CD LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1500 CD LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1500 CD LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1500 CD LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1500 CD LEU A 490 10.389 36.884 -0.181 1.00										
ATOM 1473 N GLN A 487 8.070 33.545 -3.271 1.00 44.64 ATOM 1474 CA GLN A 487 8.112 34.813 -3.998 1.00 51.86 ATOM 1475 CB GLN A 487 9.000 35.408 -6.310 1.00 61.36 ATOM 1476 CG GLN A 487 9.000 35.408 -6.310 1.00 61.53 ATOM 1477 CD GLN A 487 9.086 34.714 -7.571 1.00 65.93 ATOM 1478 OEI GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1479 NE2 GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1480 C GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1481 O GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1482 N HIS A 488 5.702 34.874 -3.741 1.00 47.07 ATOM 1483 CA HIS A 488 4.387 35.405 -3.423 1.00 48.67 ATOM 1486 CD HIS A 488 4.387 35.405 -3.423 1.00 48.67 ATOM 1486 CD HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1488 CD HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1489 NE2 HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1489 NE2 HIS A 488 0.074 35.272 -2.485 1.00 63.45 ATOM 1490 C HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1491 O HIS A 488 4.334 35.962 -1.986 1.00 49.05 ATOM 1491 O HIS A 488 4.334 35.962 -1.986 1.00 49.05 ATOM 1492 N VAL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1493 CA VAL A 489 4.755 35.154 -1.021 1.00 44.86 ATOM 1494 CB VAL A 489 5.520 34.401 1.302 1.00 46.07 ATOM 1499 N LEU A 490 6.866 36.773 0.580 1.00 43.64 ATOM 1499 N LEU A 490 6.866 36.776 0.006 1.00 43.48 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 43.48 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 43.48 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 43.49 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 43.49 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 50.68 ATOM 1504 CD2 LEU A 490 10.239 36.884 -0.181 1.00 54.04 ATOM 1504 CD2 LEU A 490 7.385 37.410 -0.766 1.00 50.68 ATOM 1507 N GLN A 491 7.014 39.243 -1.155 1.00 68.27 ATOM 1500 CB LEU A 490 7.386 39.394 -5.862 1.00 79.38 ATOM 1500 CB GLN A 491 7.014 39.243 -1.587 1.00 60.66 ATOM 1500 CB GLN A 491 7.014 39.243 -1.587 1.00 60.66 ATOM 1500 CB GLN A 491 7.034 39.394 -5.862 1.00 79.38 ATOM 1511 CD GLN A 491 7.133 40.231 -6.302 1.00 68.27										
ATOM 1474 CA GLN A 487 8.112 34.813 -3.998 1.00 47.16 ATOM 1475 CB GLN A 487 9.00 35.408 -6.310 1.00 61.53 ATOM 1477 CD GLN A 487 9.486 34.714 -7.571 1.00 65.93 ATOM 1477 CD GLN A 487 9.486 34.714 -7.571 1.00 65.93 ATOM 1479 NE2 GLN A 487 9.486 34.714 -7.571 1.00 65.93 ATOM 1479 NE2 GLN A 487 10.369 35.373 -8.311 1.00 70.60 ATOM 1480 C GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1481 O GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1482 N HIS A 488 5.702 34.874 -3.307 1.00 47.07 ATOM 1483 CA HIS A 488 4.387 35.405 -3.423 1.00 48.67 ATOM 1486 CB HIS A 488 2.095 34.484 -2.868 1.00 59.15 ATOM 1486 CD2 HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1488 CD1 HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1488 CD2 HIS A 488 1.097 35.317 -3.322 1.00 62.57 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1490 C HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1491 O HIS A 488 3.925 37.097 -1.757 1.00 48.67 ATOM 1492 N VAL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1494 CB VAL A 489 5.220 34.401 1.302 1.00 48.07 ATOM 1494 CB VAL A 489 5.522 34.911 2.692 1.00 44.85 ATOM 1499 C VAL A 489 5.522 34.911 2.692 1.00 44.85 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 49.79 ATOM 1499 O VAL A 489 5.329 37.763 0.580 1.00 43.28 ATOM 1499 N LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1499 N LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1499 O VAL A 489 5.329 37.797 -1.757 1.00 48.07 ATOM 1499 O VAL A 489 5.329 37.797 -1.757 1.00 48.07 ATOM 1490 C HIS A 488 3.912 -1.916 1.00 49.79 ATOM 1490 C HIS A 489 5.329 37.997 -1.757 1.00 48.07 ATOM 1491 CB VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1494 CB VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1496 CG2 VAL A 489 5.329 37.997 -1.757 1.00 60.66 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 54.94 ATOM 1501 CB LEU A 490 7.338 39.122 -0.310 1.00 54.70 ATOM 1500 CB LEU A 490 7.338 39.122 -0.310 1.00 54.70 ATOM 1500 CB LEU A 490 7.338 39.122 -0.310 1.00 54.79 ATOM 1500 CB GLN A 491 7.338 39.122 -0.310 1.00 54.70 ATOM 1500 CB GLN A 491 7.338 39.329 -1.555 1.00 66.67										
ATOM 1475 CB GLN A 487	ATOM									
ATOM 1476 CG GIN A 487 9.000 35.408 -6.310 1.00 61.53 ATOM 1477 CD GIN A 487 9.486 34.714 -7.571 1.00 65.93 ATOM 1478 OE1 GIN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1478 OE1 GIN A 487 10.369 35.373 -8.311 1.00 70.60 ATOM 1480 C GIN A 487 6.824 36.754 -3.307 1.00 47.05 ATOM 1481 O GIN A 487 6.824 36.754 -3.307 1.00 47.05 ATOM 1482 N HIS A 488 5.702 34.874 -3.741 1.00 47.07 ATOM 1482 N HIS A 488 4.387 35.405 -3.423 1.00 48.67 ATOM 1485 CG HIS A 488 4.387 35.405 -3.423 1.00 48.67 ATOM 1485 CG HIS A 488 1.095 34.484 -2.868 1.00 59.15 ATOM 1487 ND1 HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1490 C HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1491 O HIS A 488 3.925 37.097 -1.757 1.00 48.07 ATOM 1492 N VAL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1493 CA VAL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1494 CB VAL A 489 4.763 35.571 0.381 1.00 45.44 ATOM 1498 OC VAL A 489 4.763 35.571 0.381 1.00 46.07 ATOM 1498 OC VAL A 489 5.592 34.401 1.302 1.00 44.85 ATOM 1499 N LEU A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1498 OC VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1498 OC VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1498 OC VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1498 OC VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1498 OC VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1498 OC VAL A 489 5.582 34.911 2.692 1.00 44.85 ATOM 1498 OC VAL A 489 5.582 36.773 0.580 1.00 49.79 ATOM 1500 CB LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1500 CB LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1500 CB LEU A 490 7.865 37.763 0.103 1.00 54.10 ATOM 1500 CB LEU A 490 7.865 37.763 0.103 1.00 54.10 ATOM 1500 CB LEU A 490 7.865 37.763 0.103 1.00 54.00 ATOM 1500 CB LEU A 490 7.865 37.763 0.103 1.00 54.00 ATOM 1500 CB LEU A 490 7.865 37.763 0.103 1.00 54.00 ATOM 1500 CB LEU A 490 7.865 37.763 0.103 1.00 54.00 ATOM 1500 CB LEU A 490 7.865 37.763 0.103 1.00 54.00 ATOM 1500 CB LEU A 490 7.865 37.763 0.103 1.00 50.59 ATOM 1500 CB LEU A 490 7.865 37.763 0.103 1.00 54.00 ATOM 1500 CB LEU A	ATOM	1474	ca							
ATOM 1477 CD GLN A 487 9.886 34.714 -7.571 1.00 65.93 ATOM 1478 0E1 GLN A 487 9.083 33.587 -7.865 1.00 66.76 ATOM 1479 NE2 GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1481 O GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1481 O GLN A 487 6.824 36.754 -3.307 1.00 47.07 ATOM 1482 N HIS A 488 5.702 34.874 -3.307 1.00 47.07 ATOM 1483 CA HIS A 488 4.387 35.405 -3.423 1.00 48.67 ATOM 1485 CG HIS A 488 2.095 34.484 -2.868 1.00 59.15 ATOM 1486 CD2 HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1487 ND1 HIS A 488 1.037 35.317 -3.322 1.00 63.45 ATOM 1488 CE1 HIS A 488 0.074 35.272 -2.485 1.00 64.94 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1490 C HIS A 488 4.334 35.962 -1.986 1.00 49.05 ATOM 1491 O HIS A 488 4.334 35.962 -1.986 1.00 49.05 ATOM 1492 N VAL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1493 CA VAL A 489 4.765 35.571 0.381 1.00 45.40 ATOM 1496 CG2 VAL A 489 5.220 34.401 1.302 1.00 44.85 ATOM 1497 C VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1499 N LEU A 490 5.682 36.773 0.580 1.00 41.87 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.85 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.85 ATOM 1500 CA LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1500 CA LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1500 CA LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1500 CA LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1500 CA LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1500 CA LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1500 CG GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1500 CG GLN A 491 6.560 40.523 -3.638 1.00 75.99 ATOM 1500 CG GLN A 491 6.560 40.523 -3.638 1.00 75.99 ATOM 1500 CG GLN A 491 6.560 40.523 -3.638 1.00 75.99 ATOM 1501 CG GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 7	MOTA	1475	CB	GLN A	487					
ATOM 1477 CD GLN A 487 9.486 34.714 -7.571 1.00 65.93 ATOM 1478 OE1 GLN A 487 9.083 33.587 -7.865 1.00 67.060 ATOM 1480 C GLN A 487 10.369 35.373 -8.311 1.00 70.60 ATOM 1481 O GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1482 N HIS A 488 5.702 34.874 -3.741 1.00 47.07 ATOM 1483 CA HIS A 488 5.702 34.874 -3.741 1.00 47.07 ATOM 1485 CG HIS A 488 5.702 34.874 -3.741 1.00 47.07 ATOM 1485 CG HIS A 488 2.095 34.484 -2.868 1.00 51.50 ATOM 1486 CD2 HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1488 CE1 HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1488 CE1 HIS A 488 0.074 35.272 -2.485 1.00 64.94 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1490 C HIS A 488 3.925 37.097 -1.757 1.00 48.07 ATOM 1491 O HIS A 488 4.334 35.962 -1.986 1.00 49.05 ATOM 1492 N VAL A 489 4.763 35.571 0.381 1.00 48.07 ATOM 1493 CA VAL A 489 4.763 35.571 0.381 1.00 46.07 ATOM 1496 CG2 VAL A 489 4.763 35.571 0.381 1.00 44.85 ATOM 1497 C VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1499 N LEU A 490 5.592 34.911 2.692 1.00 44.85 ATOM 1499 N LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 7.224 40.037 0.498 1.00 50.68 ATOM 1500 CD LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1500 CB CLEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM	ATOM	1476	CG	GLN A	487	9.000	35.408			
ATOM 1478 OE1 GLN A 487				GLN A	487	9.486	34.714	-7.571		
ATOM 1479 NE2 GLN A 487						9.083	33.587	-7.865	1.00 6	5.76
ATOM 1480 C GLN A 487 6.823 35.579 -3.655 1.00 47.05 ATOM 1481 O GLN A 487 6.844 36.754 -3.307 1.00 45.17 ATOM 1482 N HIS A 488 5.702 34.874 -3.741 1.00 47.07 ATOM 1483 CA HIS A 488 5.702 34.874 -3.741 1.00 47.07 ATOM 1485 CG HIS A 488 4.387 35.405 -3.423 1.00 48.67 ATOM 1485 CG HIS A 488 2.095 34.484 -2.668 1.00 59.15 ATOM 1486 CD2 HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1487 ND1 HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1488 CE1 HIS A 488 0.074 35.272 -2.485 1.00 64.94 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1490 C HIS A 488 4.334 35.962 -1.986 1.00 49.05 ATOM 1491 O HIS A 488 3.925 37.097 -1.757 1.00 48.47 ATOM 1492 N VAL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1493 CA VAL A 489 4.763 35.571 0.381 1.00 45.44 ATOM 1494 CB VAL A 489 4.763 35.571 0.381 1.00 45.44 ATOM 1496 CG2 VAL A 489 5.592 34.901 2.692 1.00 44.85 ATOM 1499 N LEU A 489 5.592 34.901 2.692 1.00 44.85 ATOM 1499 N LEU A 489 5.582 34.901 2.692 1.00 44.85 ATOM 1499 N LEU A 489 5.682 36.773 0.580 1.00 49.79 ATOM 1499 N LEU A 489 5.319 37.741 1.229 1.00 41.76 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1504 CD2 LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1505 C LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1500 CA LEU A 490 7.338 39.122 -0.310 1.00 54.00 ATOM 1500 CB GLN A 491 7.014 39.243 -1.587 1.00 66.69 ATOM 1500 CB GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1500 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1501 CG GLN A 491 6.560 40.523 -3.638 1.00 77.00 82.32 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 77.00 82.32 ATOM 1511 CD GLN A 491 6.560 40.523 -3.663 1.00 79.38 ATOM 1512 CG GLN A 491 6.560 40.523 -3.663 1.00 79.38 ATOM 1514 C GLN A 491 6.560 40.523 -3.663 1.00 79.38 ATOM 1514 C GLN A 491 6.560 40.523 -3.663 1.00 79.38 ATOM 1514 C GLN A 491 6.560 40.523 -3.663 1.00 79.38 ATOM 1514 C GLN A 491 6.560 40.523 -3.663 1.00 79							35.373	-8.311	1.00 7	0.60
ATOM 1481 O GIN A 487 6.844 36.754 -3.307 1.00 45.17 ATOM 1482 N HIS A 488 5.702 34.874 -3.741 1.00 47.07 ATOM 1482 N HIS A 488 4.387 35.405 -3.423 1.00 48.67 ATOM 1485 CG HIS A 488 2.095 34.484 -2.868 1.00 59.15 ATOM 1485 CG HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1486 CD2 HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1488 CE1 HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1488 CE1 HIS A 488 0.074 35.272 -2.485 1.00 65.61 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1491 O HIS A 488 3.925 37.097 -1.757 1.00 48.07 ATOM 1493 CA VAL A 489 4.755 35.154 -1.021 1.00 44.07 ATOM 1493 CA VAL A 489 4.763 35.571 0.381 1.00 45.44 ATOM 1494 CB VAL A 489 4.763 35.571 0.381 1.00 44.85 ATOM 1496 CG2 VAL A 489 5.220 34.911 2.692 1.00 44.85 ATOM 1497 C VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 41.87 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 41.87 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 44.44 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 44.44 ATOM 1500 CA LEU A 490 9.075 37.410 -0.766 1.00 54.00 ATOM 1503 CD1 LEU A 490 9.075 37.410 -0.766 1.00 54.00 ATOM 1503 CD1 LEU A 490 9.075 37.410 -0.766 1.00 54.00 ATOM 1500 CA LEU A 490 9.075 37.411 1.00 54.00 ATOM 1500 CA LEU A 490 9.075 37.410 -0.766 1.00 54.00 ATOM 1500 CB LEU A 490 9.075 37.410 -0.766 1.00 54.00 ATOM 1500 CB LEU A 490 9.075 37.410 -0.766 1.00 54.00 ATOM 1500 CB LEU A 490 9.075 37.410 -0.766 1.00 54.00 ATOM 1500 CB LEU A 490 9.075 37.410 -0.766 1.00 54.00 ATOM 1500 CB GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1500 CB GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1500 CB GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 75.89 ATOM 15										
ATOM 1482 N HIS A 488										
ATOM 1483 CA HIS A 488										
ATOM 1485 CB HIS A 488 2.095 34.484 -2.868 1.00 59.15 ATOM 1486 CD2 HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1487 ND1 HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1488 CE1 HIS A 488 0.074 35.272 -2.485 1.00 64.94 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1490 C HIS A 488 3.925 37.097 -1.757 1.00 48.47 ATOM 1491 O HIS A 488 3.925 37.097 -1.757 1.00 48.47 ATOM 1492 N VAL A 489 4.755 35.154 -1.021 1.00 48.47 ATOM 1493 CB VAL A 489 4.763 35.5154 -1.021 1.00 48.07 ATOM 1494 CB VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1495 CG1 VAL A 489 4.115 33.372 1.409 1.00 41.76 ATOM 1498 O VAL A 489 4.15 33.7741 1.229 1.00 41.87 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 49.79 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1502 CG LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1504 CD2 LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1505 C LEU A 490 10.323 36.100 1.115 1.00 54.10 ATOM 1506 O LEU A 490 7.324 40.035 -1.241 1.00 54.10 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1500 CG GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1501 CG GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1501 CG GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1508 CA GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1508 CA GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1501 CG GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1501 CG GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1501 CG GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1501 CG GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1501 CG GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1501 CG GLN A 491 6.560 40.523 -3.638 1.00 72.90 ATOM 1513 CG GLN A 491 6.560 40.663 -1.555 1.00 68.27 ATOM 1514 C GGLN A 491 6.560 40.663 -1.555 1.00 68.27	MOTA	1482								
ATOM 1485 CG HIS A 488	MOTA	1483	CA							
ATOM 1485 CG HIS A 488 2.095 34.484 -2.868 1.00 59.15 ATOM 1486 CD2 HIS A 488 1.638 33.939 -1.715 1.00 62.57 ATOM 1487 ND1 HIS A 488 1.097 35.317 -3.322 1.00 63.45 ATOM 1488 CE1 HIS A 488 0.074 35.272 -2.485 1.00 64.94 ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1491 O HIS A 488 4.334 35.962 -1.986 1.00 49.05 ATOM 1492 N VAL A 489 4.755 35.154 -1.021 1.00 48.47 ATOM 1493 CA VAL A 489 4.763 35.571 0.381 1.00 45.44 ATOM 1494 CB VAL A 489 4.763 35.571 0.381 1.00 45.44 ATOM 1495 CG1 VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1496 CG2 VAL A 489 4.115 33.372 1.409 1.00 41.76 ATOM 1497 C VAL A 489 4.115 33.372 1.409 1.00 41.76 ATOM 1498 N LEU A 490 5.682 36.773 0.580 1.00 43.28 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1502 CG LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1504 CD2 LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1505 C LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1508 CA GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1509 CB GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1512 OCI GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1513 NE2 GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1513 NE2 GLN A 491 6.560 40.523 -3.638 1.00 77.38 ATOM 1514 C GLN A 491 6.560 40.523 -3.638 1.00 79.38 ATOM 1513 NE2 GLN A 491 6.560 40.523 -3.6647 1.00 68.27	ATOM	1484	CB	HIS A	488					
ATOM 1486 CD2 HIS A 488		1485	CG	HIS A	488	2.095				
ATOM 1487 ND1 HIS A 488			CD2	HIS A	488	1.638	33.939	-1.715		
ATOM 1488 CE1 HIS A 488						1.097	35.317	-3.322	1.00 6	3.45
ATOM 1489 NE2 HIS A 488 0.378 34.444 -1.500 1.00 65.61 ATOM 1490 C HIS A 488 4.334 35.962 -1.986 1.00 49.05 ATOM 1491 O HIS A 488 3.925 37.097 -1.757 1.00 48.07 ATOM 1492 N VAL A 489 4.763 35.571 0.381 1.00 45.44 ATOM 1493 CA VAL A 489 4.763 35.571 0.381 1.00 45.44 ATOM 1494 CB VAL A 489 5.220 34.401 1.302 1.00 46.07 ATOM 1495 CGI VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1496 CG2 VAL A 489 4.115 33.372 1.409 1.00 41.76 ATOM 1497 C VAL A 489 5.682 36.773 0.580 1.00 43.28 ATOM 1498 O VAL A 489 5.682 36.773 0.580 1.00 43.28 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CA LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CB LEU A 490 9.075 37.410 -0.766 1.00 49.79 ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 50.68 ATOM 1502 CG LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1505 C LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1507 N GLN A 491 7.338 39.122 -0.310 1.00 52.92 ATOM 1508 CA GLN A 491 7.014 39.243 -1.587 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM						0.074	35,272	-2.485	1.00 6	4.94
ATOM 1490 C HIS A 488								-1.500	1.00 6	5.61
ATOM 1491 O HIS A 488 3.925 37.097 -1.757 1.00 48.47 ATOM 1492 N VAL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1493 CA VAL A 489 4.763 35.571 0.381 1.00 45.44 ATOM 1494 CB VAL A 489 5.220 34.401 1.302 1.00 46.07 ATOM 1495 CG1 VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1496 CG2 VAL A 489 4.115 33.372 1.409 1.00 41.76 ATOM 1497 C VAL A 489 5.682 36.773 0.580 1.00 43.28 ATOM 1498 O VAL A 489 5.319 37.741 1.229 1.00 41.87 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 50.68 ATOM 1502 CG LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1504 CD2 LEU A 490 10.389 36.884 -0.181 1.00 54.10 ATOM 1506 O LEU A 490 11.034 36.035 -1.241 1.00 54.10 ATOM 1506 O LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 52.92 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1509 CB GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514									1.00 4	9.05
ATOM 1492 N VAL A 489 4.755 35.154 -1.021 1.00 48.07 ATOM 1493 CA VAL A 489 4.763 35.571 0.381 1.00 45.44 ATOM 1494 CB VAL A 489 5.220 34.401 1.302 1.00 46.07 ATOM 1496 CG2 VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1496 CG2 VAL A 489 4.115 33.372 1.409 1.00 41.76 ATOM 1497 C VAL A 489 5.682 36.773 0.580 1.00 43.28 ATOM 1498 O VAL A 489 5.682 36.773 0.580 1.00 43.28 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 50.68 ATOM 1502 CG LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1504 CD2 LEU A 490 10.223 36.100 1.115 1.00 54.10 ATOM 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.338 39.122 -0.310 1.00 52.59 ATOM 1507 N GLN A 491 7.338 39.122 -0.310 1.00 52.59 ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82										
ATOM 1493 CA VAL A 489										
ATOM 1494 CB VAL A 489 5.220 34.401 1.302 1.00 46.07 ATOM 1495 CG1 VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1496 CG2 VAL A 489 4.115 33.372 1.409 1.00 41.76 ATOM 1497 C VAL A 489 5.682 36.773 0.580 1.00 43.28 ATOM 1498 O VAL A 489 5.319 37.741 1.229 1.00 41.87 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 50.68 ATOM 1503 CD1 LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.223 36.100 1.115 1.00 54.10 ATOM 1504 CD2 LEU A 490 11.034 36.035 -1.241 1.00 54.10 ATOM 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1509 CB GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1510 CG GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27 ATOM 1514 C										
ATOM 1495 CG1 VAL A 489 5.592 34.911 2.692 1.00 44.85 ATOM 1496 CG2 VAL A 489 4.115 33.372 1.409 1.00 41.76 ATOM 1497 C VAL A 489 5.682 36.773 0.580 1.00 43.28 ATOM 1498 O VAL A 489 5.319 37.741 1.229 1.00 41.87 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 50.68 ATOM 1502 CG LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.223 36.100 1.115 1.00 54.10 ATOM 1504 CD2 LEU A 490 11.034 36.035 -1.241 1.00 54.17 ATOM 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1509 CB GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1500 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OEI GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.276	ATOM					4.763				
ATOM 1496 CG2 VAL A 489	ATOM	1494								
ATOM 1497 C VAL A 489 5.682 36.773 0.580 1.00 43.28 ATOM 1498 O VAL A 489 5.319 37.741 1.229 1.00 41.87 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 50.68 ATOM 1502 CG LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.223 36.100 1.115 1.00 54.10 ATOM 1504 CD2 LEU A 490 11.034 36.035 -1.241 1.00 54.17 ATOM 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27	MOTA	1495	CG1	VAL A	489					
ATOM 1497 C VAL A 489 5.682 36.773 0.580 1.00 43.28 ATOM 1498 O VAL A 489 5.319 37.741 1.229 1.00 41.87 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1504 CD2 LEU A 490 11.034 36.035 -1.241 1.00 54.10 ATOM 1505 C LEU A 490 11.034 36.035 -1.241 1.00 54.10 ATOM 1506 O LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1509 CB GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1512 OE1 GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1513 NE2 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 60.66 326	ATOM	1496	CG2	VAL A	489					
ATOM 1498 O VAL A 489 5.319 37.741 1.229 1.00 41.87 ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 50.68 ATOM 1503 CD1 LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1504 CD2 LEU A 490 10.223 36.100 1.115 1.00 54.10 ATOM 1505 C LEU A 490 11.034 36.035 -1.241 1.00 54.17 ATOM 1506 O LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1509 CB GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1512 OE1 GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1513 NE2 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 60.26 1.00 60.36		1497	C	VAL A	489	5.682	36.773	0.580	1.00 4	3.28
ATOM 1499 N LEU A 490 6.866 36.706 -0.006 1.00 44.44 ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 50.68 ATOM 1502 CG LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.223 36.100 1.115 1.00 54.10 ATOM 1504 CD2 LEU A 490 11.034 36.035 -1.241 1.00 54.17 ATOM 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27				VAL A	489	5.319	37.741	1.229		
ATOM 1500 CA LEU A 490 7.865 37.763 0.103 1.00 49.79 ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 50.68 ATOM 1502 CG LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.223 36.100 1.115 1.00 54.10 ATOM 1504 CD2 LEU A 490 11.034 36.035 -1.241 1.00 54.17 ATOM 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 68.27						6.866	36.706	-0.006	1.00 4	4.44
ATOM 1501 CB LEU A 490 9.075 37.410 -0.766 1.00 50.68 ATOM 1502 CG LEU A 490 10.389 36.884 -0.181 1.00 54.00 ATOM 1503 CD1 LEU A 490 10.223 36.100 1.115 1.00 54.10 ATOM 1504 CD2 LEU A 490 11.034 36.035 -1.241 1.00 54.17 ATOM 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.672 38.554 -6.647 1.00 66.27									1.00 4	9.79
ATOM 1502 CG LEU A 490 10.389 36.884 -0.181 1.00 54.00 1503 CD1 LEU A 490 10.223 36.100 1.115 1.00 54.10 1504 CD2 LEU A 490 11.034 36.035 -1.241 1.00 54.17 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 1500 1506 O LEU A 490 7.338 39.122 -0.310 1.00 52.92 1500 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 1500 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 1510 CG GLN A 491 6.340 39.394 -5.862 1.00 79.38 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 1514 C GLN A 491 5.672 38.554 -6.647 1.00 81.82 1514 C GLN A 491 5.672 38.554 -6.647 1.00 69.36							37 410			
ATOM 1503 CD1 LEU A 490 10.223 36.100 1.115 1.00 54.10 ATOM 1504 CD2 LEU A 490 11.034 36.035 -1.241 1.00 54.17 ATOM 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.078 39.292 -4.373 1.00 75.89 ATOM 1512 OE1 GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1513 NE2 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27								-		
ATOM 1504 CD2 LEU A 490 11.034 36.035 -1.241 1.00 54.17 ATOM 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1510 CG GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1511 CD GLN A 491 6.078 39.292 -4.373 1.00 75.89 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27										
ATOM 1505 C LEU A 490 7.338 39.122 -0.310 1.00 52.92 ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.078 39.292 -4.373 1.00 75.89 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27	ATOM									
ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.078 39.292 -4.373 1.00 75.89 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27	ATOM		CD2							
ATOM 1506 O LEU A 490 7.224 40.037 0.498 1.00 50.59 ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.078 39.292 -4.373 1.00 75.89 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27	ATOM	1505	С						1.00 5	2.92
ATOM 1507 N GLN A 491 7.014 39.243 -1.587 1.00 60.06 ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.078 39.292 -4.373 1.00 75.89 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27		1506	0	LEU A	490		40.037			
ATOM 1508 CA GLN A 491 6.513 40.494 -2.107 1.00 66.69 ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.078 39.292 -4.373 1.00 75.89 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27						7.014	39.243			
ATOM 1509 CB GLN A 491 6.560 40.523 -3.638 1.00 72.00 ATOM 1510 CG GLN A 491 6.078 39.292 -4.373 1.00 75.89 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27						6.513		-2.107		
ATOM 1510 CG GLN A 491 6.078 39.292 -4.373 1.00 75.89 ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27									1.00 7	2.00
ATOM 1511 CD GLN A 491 6.340 39.394 -5.862 1.00 79.38 ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27										
ATOM 1512 OE1 GLN A 491 7.133 40.231 -6.302 1.00 82.32 ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27										
ATOM 1513 NE2 GLN A 491 5.672 38.554 -6.647 1.00 81.82 ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27										
ATOM 1514 C GLN A 491 5.144 40.863 -1.555 1.00 68.27				. GLW A	471					
4 000 40 045 1 427 1 00 60 36							40 04°			
ATOM 1515 O GLN A 491 4.820 42.045 -1.433 1.00 69.36										
	MOTA	1515	O	GLN A	491	4.820	42.043	-1.433	1.00 6	J.30

- 55 -

				400	4 260	39.863	-1.168	1.00 69.33
ATOM	1516	N	LYS A	492	4.360	40.123	-0.581	1.00 70.57
ATOM	1517	CA	LYS A	492	3.055			1.00 63.87
ATOM	1518	CB	LYS A	492	2.464	38.825	-0.036	1.00 55.18
ATOM	1519	CG	LYS A		1.419	39.011	1.021	
ATOM	1520	CD	LYS A		0.936	37.684	1.518	1.00 50.15
ATOM	1521	CE	LYS A	492	0.170	36.960	0.445	1.00 47.92
ATOM	1522	NZ	LYS A		-0.429	35.700	0.955	1.00 49.79
ATOM	1523	c	LYS A	492	3.258	41.101	0.561	1.00 76.10
	1524	ŏ	LYS A	492	2.447	41.991	0.778	1.00 78.57
MOTA	1525	N	ASN A		4.387	40.955	1.245	1.00 83.09
MOTA			ASN A		4.724	41.795	2.380	1.00 90.65
MOTA	1526	CA	ASN A	493	5.326	40.936	3.510	1.00 91.76
MOTA	1527	CB			4.413	39.791	3.960	1.00 91.33
MOTA	1528	CG	ASN A			39.989	4.743	1.00 90.45
MOTA	1529	ODT	ASN A	493	3.483		3.525	1.00 90.60
MOTA	1530		ASN A	493	4.727	38.576	2.053	1.00 96.54
ATOM	1531	С	ASN A	493	5.703	42.929	2.361	1.00 97.40
ATOM	1532	0	ASN A		5.445	44.097		1.00104.63
ATOM	1533	N	HIS A		6.815	42.593	1.401	
ATOM	1534	CA	HIS A	494	7.847	43.592	1.111	1.00112.99
ATOM	1535	CB	HIS A	494	9.092	43.302	1.972	1.00118.20
ATOM	1536	CG	HIS A		8.776	42.865	3.375	1.00123.22
ATOM	1537	CD2	HIS A	494	8.606	41.630	3.906	1.00124.65
ATOM	1538		HIS A	494	8.580	43.754	4.409	1.00125.31
ATOM	1539	CEI	HIS A	494	8.306	43.087	5.517	1.00125.71
ATOM	1540	NE2	HIS A	494	8.314	41.796	5.238	1.00124.45
	1541	C	HIS A	494	8.283	43.810	-0.343	1.00115.21
MOTA	1542	ŏ	HIS A		9.414	43.476	-0.719	1.00113.88
MOTA			ARG A		7.411	44.411	-1.150	1.00118.74
ATOM	1543	N	ARG A		7.771	44.693	-2.539	1.00123.08
ATOM	1544	CA	ARG A	495	6.532	44.895	-3.411	1.00124.19
MOTA	1545	CB			5.922	43.611	-3.923	1.00125.95
MOTA	1546	CG	ARG A		4.905	43.869	-5.022	1.00128.86
MOTA	1547	CD	ARG A			42.688	-5.336	1.00130.65
MOTA	1548	NE	ARG A	495	4.097		-5.469	1.00131.44
ATOM	1549	CZ	ARG A	495	2.771	42.700	-5.316	1.00132.26
ATOM	1550	NHI		495	2.089	43.829	-5.755	1.00132.05
ATOM	1551	NH2			2.122	41.580		1.00132.03
ATOM	1552	С	ARG A		8.677	45.927	-2.632	1.00124.82
ATOM	1553	0	ARG A		9.086	46.332	-3.723	
ATOM	1554	N	GLU A	496	8.979	46.520	-1.479	1.00125.27
ATOM	1555	CA	GLU A		9.840	47.694	-1.403	1.00125.62
ATOM	1556	CB	GLU A	496	10.086	48.053	0.060	1.00125.24
ATOM	1557	CG	GLU A	496	10.364	46.856	0.953	1.00125.43
ATOM	1558	CD	GLU A		10.161	47.175	2.414	1.00127.70
ATOM	1559	OE1	GLU A	496	11.014	47.880	2.992	1.00129.15
ATOM	1560	OE2			9.137	46.733	2.981	1.00127.94
MOTA	1561	C	GLU A	496	11.162	47.439	-2.117	1.00126.43
ATOM	1562	Ö	GLU A	496	11.731	48.346	-2.723	1.00127.96
	1563	N	ASP A	497	11.635	46.195	-2.047	1.00126.16
MOTA	1564	CA	ASP A	497	12.886	45.790	-2.693	1.00124.22
MOTA	1565	CB	ASP A	497	14.036	45.643	-1.669	1.00124.95
ATOM		CG	ASP A	197	13.719	46.260	-0.317	1.00125.55
ATOM	1566	001	L ASP A	197	13.970	47.468	-0.132	1.00125.55
ATOM	1567	ישט.	ASP A	107	13.221	45.530	0.565	1.00126.80
ATOM	1568		ASP A	1 427	12.646	44.446	-3.392	1.00121.48
MOTA	1569	C	ASP 7	1 497	11.524	44.142	-3.807	1.00121.28
MOTA	1570	0	ASP A			43.655	-3.527	1.00118.36
MOTA	1571	N	GLY A		13.711	42.337	-4.142	1.00112.17
MOTA	1572	CA	GLY A		13.637			1.00106.96
MOTA	1573	С		4 498	14.617	41.465	-3.374	1.00107.39
MOTA	1574	О	GLY A	498	15.677	41.104	-3.889	1.00100.38
MOTA	1575	N	ILE A	A 499	14.253	41.158	-2.128	1.00100.38
ATOM	1576	CA	ILE A	A 499	15.058	40.378	-1.187	
MOTA	1577	CB		A 499	14.545	40.644		1.00 89.37
ATOM	1578	CG	2 ILE 2	A 499	14.172	39.362	0.988	1.00 88.94
MOTA	1579	CG:	1 ILE A	A 499	15.573	41.483	1.013	1.00 88.59
MOTA	1580	CD	1 ILE A		16.015	42.736	0.254	1.00 88.83
ATOM	1581	С	ILE A	A 499	15.254	38.885	-1.469	1.00 85.97

3 mOM	1582	0	ILE A 499	16.120	38.243	-0.872	1.00	81.39
ATOM		И	LEU A 500	14.482	38.353	-2.412	1.00	82.32
MOTA	1583		LEU A 500	14.572	36.945	-2.784	1.00	79.33
MOTA	1584	CA	DEU A 500	13.593	36.610	-3.926		75.45
MOTA	1585	CB	LEU A 500			-4.427		72.35
MOTA	1586	CG	LEU A 500	13.480	35.160			
ATOM	1587	CD1	LEU A 500	13.020	34.209	-3.345		70.46
ATOM	1588	CD2	LEU A 500	12.509	35.104	-5.569		74.01
MOTA	1589	C	LEU A 500	15.994	36.594	-3.191		78.86
	1590	ŏ	LEU A 500	16.443	35.483	-2.943	1.00	80.08
MOTA		N	THR A 501	16.709	37.548	-3.786	1.00	78.15
MOTA	1591		THR A 501	18.085	37.316	-4.224	1.00	79.02
MOTA	1592	CA		18.654	38.487	-5.065		82.06
MOTA	1593	CB	THR A 501		39.635	-4.225		84.30
MOTA	1594	OG1		18.870		-6.214		83.64
MOTA	1595	CG2	THR A 501	17.708	38.834			77.23
MOTA	1596	C	THR A 501	18.935	37.193	-2.988		
ATOM	1597	0	THR A 501	19.694	36.236	-2.831		77.82
ATOM	1598	N	LYS A 502	18.776	38.185	-2.117		74.83
ATOM	1599	CA	LYS A 502	19.478	38.276	-0.847		72.92
ATOM	1600	CB	LYS A 502	18.834	39.402	-0.025	1.00	79.85
	1601	CG	LYS A 502	19.726	40.108	0.995	1.00	85.84
MOTA			LYS A 502	18.937	41.231	1.690	1.00	89.85
MOTA	1602	CD		19.744	41.963	2.764		94.60
MOTA	1603	CE	LYS A 502	18.918	42.984	3.487		95.90
MOTA	1604	NZ	LYS A 502			-0.158		66.91
MOTA	1605	С	LYS A 502	19.282	36.922			65.72
MOTA	1606	0	LYS A 502	20.227	36.332	0.360		
ATOM	1607	N	LEU A 503	18.060	36.409	-0.267		59.20
ATOM	1608	CA	LEU A 503	17.662	35.134	0.306		52.88
ATOM	1609	CB	LEU A 503	16.158	34.971	0.156		47.50
MOTA	1610	CG	LEU A 503	15.466	34.377	1.365	1.00	
ATOM	1611	CD1		16.066	34.928	2.664		46.78
ATOM	1612	CD2		13.990	34.688	1.270		51.22
	1613	C	LEU A 503	18.374	33.938	-0.314	1.00	51.55
MOTA		Ö	LEU A 503	19.200	33.301	0.334	1.00	49.38
MOTA	1614		ILE A 504	18.087	33.645	-1.579	1.00	50.92
ATOM	1615	N	ILE A 504	18.715	32.499	-2.231		51.60
ATOM	1616	ĊĀ		18.054	32.153	-3.588	1.00	55.42
ATOM	1617	CB	ILE A 504	16.718	31.464	-3.360		52.28
MOTA	1618	CG2			33.415	-4.418		59.46
ATOM	1619	CG1		17.860		-5.320		67.68
MOTA	1620	CD1		16.623	33.368			49.75
ATOM	1621	C	ILE A 504	20.233	32.598	-2.336		50.38
ATOM	1622	0	ILE A 504	20.917	31.593	-2.485		
MOTA	1623	N	CYS A 505	20.773	33.798	-2.192	1.00	
ATOM	1624	CA	CYS A 505	22.221	33.974	-2.220	1.00	
ATOM	1625	CB	CYS A 505	22.557	35.465	-2.457	1.00	58.96
ATOM	1626	SG	CYS A 505	23.762	36.304	-1.354	1.00	
ATOM	1627	C	CYS A 505	22.791	33.433	-0.891	1.00	
MOTA	1628	ō	CYS A 505	23.956	33.014	-0.803		41.30
	1629	N	LYS A 506	21.939	33.398	0.131	1.00	40.06
MOTA	1630	CA	LYS A 506	22.336	32.890	1.425	1.00	37.35
MOTA			LYS A 506	21.286	33.221	2.481	1.00	40.11
MOTA	1631	CB	LYS A 506	20.957	34.686	2.596	1.00	43.49
ATOM	1632	CG	TYC 7 EOC	22.217	35.514	2.611	1.00	51.34
ATOM	1633	CD	LYS A 506	22.343	36.269	3.891	1 00	55.65
MOTA	1634	CE	LYS A 506		35.376	5.071		63.77
MOTA	1635	NZ	LYS A 506	22.139				36.27
ATOM	1636	C	LYS A 506	22.466	31.389	1.309		
MOTA	1637	0	LYS A 506	23.267	30.786	2.005	1.00	40.04
ATOM	1638	N	VAL A 507	21.692	30.784	0.417		32.90
ATOM	1639	CA	VAL A 507	21.735	29.341	0.227		35.32
ATOM	1640	СВ	VAL A 507	20.809	28.932	-0.926		39.14
ATOM	1641	CG1	L VAL A 507	20.872	27.438	-1.155	1.00	41.89
ATOM	1642	CG	2 VAL A 507	19.382	29.364	-0.630		35.73
ATOM	1643	c	VAL A 507	23.146	28.782	-0.016		35.01
ATOM	1644	ŏ	VAL A 507	23.447	27.642	0.318	1.00	
ATOM	1645	N	SER A 508	24.009	29.584	-0.616	1.00	36.29
	1646	CA	SER A 508	25.372	29.159	-0.886	1.00	37.66
MOTA	1647	CB	SER A 508	25.996	30.084	-1.941		38.93
MOTA	104/	CB	DEK A JOU	24.550				

ATOM	1648	OG	SER A 5	ហន	27.309	29.693	-2.294	1.00	45.66
ATOM	1649	C	SER A 5		26.192	29.172	0.420	1.00	37.79
	1650	Ö	SER A 5		27.026	28.280	0.647		37.44
ATOM			THR A 5		25.949	30.178	1.267		35.49
ATOM	1651	N	THR A 5		26.627	30.326	2.553		32.31
ATOM	1652	CA			26.250	31.644	3.236		35.78
MOTA	1653	CB	THR A 5	509			2.305		42.43
MOTA	1654	OG1	THR A 5		26.405	32.720			35.82
ATOM	1655	CG2	THR A 5		27.157	31.895	4.437		
ATOM	1656	С	THR A 5		26.231	29.187	3.469		28.28
MOTA	1657	0	THR A 5	509	27.065	28.665	4.178		32.41
ATOM	1658	N	LEU A 5	510	24.958	28.812	3.452		28.16
MOTA	1659	CA	LEU A 5	510	24.452	27.696	4.249		29.00
ATOM	1660	CB	LEU A 5		22.994	27.394	3.885		26.48
ATOM	1661	CG	LEU A 5		21.819	28.079	4.571	1.00	29.80
ATOM	1662	CD1	_		20.544	27.623	3.907	1.00	28.25
ATOM	1663	CD2	_		21.793	27.717	6.063	1.00	30.36
ATOM	1664	C	LEU A 5		25.267	26.437	3.969	1.00	32.43
	1665	ŏ	LEU A 5		25.639	25.698	4.885	1.00	32.33
ATOM	1666	N	ARG A		25.524	26.194	2.685		31.40
ATOM		CA	ARG A		26.272	25.027	2.233		28.94
ATOM	1667		ARG A		26.170	24.909	0.706		34.59
ATOM	1668	CB			24.716	24.741	0.261		34.26
MOTA	1669	CG	ARG A			24.611	-1.225		36.35
MOTA	1670	CD	ARG A	244 2TT	24.547		-1.556	1 00	31.13
MOTA	1671	NE	ARG A	2 T T	23.192	24.185			31.68
MOTA	1672	CZ	ARG A		22.887	23.356	-2.545		32.54
MOTA	1673	NH1			23.839	22.856	-3.324		27.68
MOTA	1674	NH2			21.628	23.004	-2.730		
MOTA	1675	C	ARG A		27.710	25.049	2.695		26.34
ATOM	1676	0	ARG A		28.270	24.011	3.015		28.74
MOTA	1677	N	ALA A S	512	28.314	26.235	2.693		25.39
ATOM	1678	CA	ALA A	512	29.687	26.409	3.161		24.68
ATOM	1679	CB	ALA A!		30.157	27.796	2.830		22.96
ATOM	1680	С	ALA A	512	29.732	26.195	4.691		27.69
MOTA	1681	0	ALA A	512	30.622	25.518	5.231		27.18
MOTA	1682	ĨĨ	LEU A		28.773	26.814	5.373	1.00	27.16
ATOM	1683	CA	LEU A !		28.638	26.708	6.815		26.64
MOTA	1684	CB	LEU A		27.427	27.528	7.256	1.00	24.45
ATOM	1685	ĊĠ	LEU A		27.228	27.696	8.758	1.00	28.40
ATOM	1686	CD1			28.492	28.230	9.403	1.00	25.85
ATOM	1687	CD2			26.053	28.607	9.013	1.00	30.72
ATOM	1688	C	LEU A		28.490	25.209	7.192	1.00	29.10
ATOM	1689	ŏ	LEU A		29.259	24.683	8.008	1.00	31.91
ATOM	1690	Ŋ	CYS A		27.543	24.512	6.566	1.00	26.57
ATOM	1691	CA	CYS A		27.351	23.104	6.851	1.00	26.98
	1692	CB	CYS A		26.025	22.614	6.269	1.00	
ATOM	1693	SG	CYS A		24.579	23.438	7.009		30.96
ATOM ATOM	1694	C	CYS A		28.538	22.250	6.404		28.07
			CYS A	51 <i>4</i>	28.764	21.161	6.931		27.30
MOTA	1695	O	GLY A	J14 515	29.298	22.741	5.431		29.78
MOTA	1696	N	GLY A	515 515	30.477	22.027	4.980		29.40
ATOM	1697	CA			31.570	22.004	6.040		30.10
ATOM	1698	C	GLY A			20.965	6.266		30.71
ATOM	1699	0	GLY A	212	32.190		6.693		33.97
MOTA	1700	N	ARG A	210	31.810	23.142			34.03
MOTA	1701	CA	ARG A	516	32.811	23.217	7.748		
MOTA	1702	CB	ARG A		33.065	24.652	8.178		37.07
MOTA	1703	CG	ARG A	516	33.921	25.429	7.198		52.01
ATOM	1704	CD	ARG A	516	34.465	26.715	7.807		56.98
ATOM	1705	NE	ARG A	516	35.467	26.438	8.836		61.64
MOTA	1706	CZ	ARG A		35.927	27.342	9.699		62.65
ATOM	1707	NH1	ARG A	516	35.466	28:590	9.665		61.40
MOTA	1708	NH2		516	36.879	27.005	10.566		60.38
MOTA	1709	С	ARG A	516	32.380	22.395	8.947		33.89
MOTA	1710	0	ARG A	516	33.227	21.847	9.634		33.31
ATOM	1711	N	HIS A	517	31.075	22.322	9.215		33.19
ATOM	1712	CA	HIS A	517	30.616	21.517	10.337		34.62
MOTA	1713	CB	HIS A		29.085	21.466	10.440	1.00	34.29

ATOM	1714	CG	HIS A	517	28.576	20.462	11.440	1.00 33.44
	1715		HIS A		28.646	20.433	12.793	1.00 31.33
ATOM	1716		HIS A		27.909	19.311	11.072	1.00 28.67
MOTA			HIS A		27.589	18.619	12.151	1.00 27.08
MOTA	1717				28.027	19.279	13.208	1.00 28.43
MOTA	1718	NE2	HIS A	2T /	31.147	20.107	10.127	1.00 36.73
ATOM	1719		HIS A		-	19.567	10.994	1.00 34.74
MOTA	1720		HIS A		31.825	19.507	8.950	1.00 36.75
ATOM	1721		THR A		30.884	19.541		1.00 36.73
ATOM	1722	CA	THR A	518	31.343	18.192	8.662	
ATOM	1723		THR A		30.692	17.620	7.406	1.00 35.05
ATOM	1724		THR A		29.327	17.303	7.688	1.00 37.15
ATOM	1725	CG2	THR A	518	31.382	16.346	6.980	1.00 38.73
ATOM	1726	С	THR A	518	32.862	18.100	8.608	1.00 37.39
ATOM	1727	0	THR A	518	33.430	17.077	8.962	1.00 42.45
ATOM	1728	N	GLU A		33.531	19.175	8.220	1.00 38.67
ATOM	1729	CA	GLU A		34.990	19.166	8.196	1.00 43.58
ATOM	1730	CB	GLU A		35.516	20.438	7.500	1.00 54.27
ATOM	1731	CG	GLU A		35.261	20.537	5.964	1.00 63.20
ATOM	1732	CD	GLU A		35.380	21.975	5.406	1.00 65.12
	1733	OE1	GLU A		34.782	22.258	4.342	1.00 66.49
MOTA			GLU A		36.053	22.826	6.035	1.00 67.73
MOTA	1734		GLU A		35.516	19.099	9.649	1.00 42.46
MOTA	1735	C	GLU A		36.470	18.382	9.959	1.00 39.74
MOTA	1736	0	LYS A	273	34.857	19.843	10.535	1.00 41.75
ATOM	1737	N	LYS A	520	35.222	19.895	11.945	1.00 37.07
ATOM	1738	CA	LYS A		34.481	21.049	12.651	1.00 41.10
ATOM	1739	CB	LYS A			22.467	12.235	1.00 44.66
MOTA	1740	CG	LYS A	520	34.939		12.670	1.00 53.92
MOTA	1741	CD	LYS A		36.383	22.748	11.819	1.00 56.95
ATOM	1742	CE	LYS A		37.078	23.819		1.00 63.31
ATOM	1743	NZ	LYS A		37.313	23.411	10.388	1.00 33.31
ATOM	1744	C	LYS A		34.911	18.560	12.618	
ATOM	1745	0	LYS A		35.770	17.983	13.278	
MOTA	1746	N	LEU A		33.703	18.051	12.394	1.00 33.45
ATOM	1747	CA	LEU A		33.270	16.782	12.956	1.00 33.31
ATOM	1748	CB	LEU A		31.839	16.460	12.526	1.00 26.37
ATOM	1749	CG	LEU A	521	31.268	15.095	12.905	1.00 24.78
ATOM	1750	CD1	LEU A	521	31.380	14.865	14.394	1.00 29.22
ATOM	1751	CD2			29.832	15.021	12.520	1.00 24.85
ATOM	1752	С	LEU A	521	34.214	15.633	12.601	1.00 38.43
ATOM	1753	0	LEU A		34.564	14.843	13.477	1.00 38.10
ATOM	1754	N	MET A	522	34.694	15.581	11.356	1.00 39.97
ATOM	1755	CA	MET A	522	35.601	14.507	10.947	1.00 41.97
ATOM	1756	CB	MET A	522	35.725	14.431	9.426	1.00 48.01
ATOM	1757	CG	MET A		34.430	14.035	8.707	1.00 58.55
ATOM	1758	SD	MET A		33.355	12.804	9.548	1.00 67.62
ATOM	1759	CE	MET A	522	34.455	11.351	9.732	1.00 65.55
ATOM	1760	Č	MET A	522	36.982	14.574	11.596	1.00 40.03
ATOM	1761	ŏ	MET A	522	37.578	13.539	11.900	1.00 37.83
ATOM	1762	Ň	ALA A	523	37.497	15.782	11.798	1.00 37.94
ATOM	1763	ĈA	ALA A	523	38.790	15.936	12.452	1.00 39.72
	1764	CB	ALA A		39.272	17.353	12.304	1.00 45.50
MOTA ATOM	1765	C	ALA A		38.640	15.587	13.938	1.00 41.81
	1766	ŏ	ALA A		39.523	14.997	14.547	1.00 44.06
MOTA		Ŋ	PHE A		37.509	15.971	14.519	1.00 41.49
ATOM	1767		PHE A	524	37.238	15.674	15.915	1.00 39.19
MOTA	1768	CA			35.923	16.334	16.360	1.00 35.12
MOTA	1769	CB	PHE A	524	35.511	15.998	17.781	1.00 30.17
ATOM	1770	CG CD1	PUE A	. J44 52/	35.968	16.762	18.852	1.00 28.22
ATOM	1771	CDT	PHE A	. 324 531	34.644	14.924	18.040	1.00 26.69
MOTA	1772	CDZ	PHE A	. 324 52 <i>1</i>	35.569	16.465	20.166	1.00 25.14
ATOM	1773		PHE A		34.240	14.620	19.341	1.00 27.45
ATOM	1774	CE2	PHE A	524		15.398	20.408	1.00 25.33
MOTA	1775	CZ	PHE A	524	34.709	14.157	16.093	1.00 38.05
ATOM	1776	C	PHE A	524	37.151	13.602	16.989	1.00 39.38
ATOM	1777	0	PHE A	525	37.788	13.602	15.240	1.00 33.74
ATOM	1778	N	LYS A	525	36.370	12.053	15.240	1.00 33.74
ATOM	1779	CA	LYS A	545	36.188	12.053		J. 00 JZ.20

MOTA	1780	CB	LYS A	525	35.150	11.566	14.341	1.00 32.43
ATOM	1781	CG	LYS A		35.058	10.061	14.265	1.00 32.27
ATOM	1782	CD	LYS A	525	34.049	9.588	13.234	1.00 39.70
ATOM	1783	CE	LYS A		34.182	8.085	13.027	1.00 43.60
ATOM	1784	NZ	LYS A		33.052	7.475	12.274	1.00 52.36
ATOM	1785	C	LYS A		37.486	11.292	15.141	1.00 37.02
ATOM	1786	ŏ	LYS A	525	37.572	10.113	15.458	1.00 38.38
ATOM	1787	Ŋ	ALA A		38.514	11.972	14.651	1.00 38.57
ATOM	1788	CA	ALA A		39.796	11.312	14.442	1.00 42.31
ATOM	1789	CB	ALA A		40.639	12.098	13.429	1.00 42.02
ATOM	1790	C	ALA A	526	40.523	11.230	15.774	1.00 43.27
ATOM	1791	Õ	ALA A	526	41.174	10.226	16.091	1.00 43.91
ATOM	1792	N	ILE A	527	40.348	12.293	16.555	1.00 41.76
ATOM	1793	CA	ILE A	527	40.961	12.455	17.866	1.00 40.21
ATOM	1794	CB	ILE A	527	41.127	13.946	18.166	1.00 40.67
ATOM	1795	CG2	ILE A	527	41.824	14.145	19.503	1.00 42.82
ATOM	1796	CG1	ILE A	527	41.897	14.612	17.026	1.00 39.18
ATOM	1797	CD1		527	41.864	16.128	17.066	1.00 37.42
MOTA	1798	C	ILE A		40.195	11.786	19.015	1.00 38.56
ATOM	1799	0		527	40.800	11.309	19.974	1.00 38.98
MOTA	1800	N	TYR A		38.871	11.727	18.900	1.00 34.57
MOTA	1801	CA	TYR A		38.023	11.135	19.930	1.00 31.38
MOTA	1802	CB	TYR A	528	37.209	12.229	20.645	1.00 31.31
MOTA	1803	CG	TYR A		38.046	13.379	21.159	1.00 34.92
MOTA	1804	CD1		528	38.337	14.471	20.345	1.00 34.80 1.00 39.08
MOTA	1805	CE1			39.157	15.513	20.789	1.00 39.08 1.00 34.45
ATOM	1806	CD2	TYR A	528	38.592	13.355	22.442	1.00 34.43
ATOM	1807	CE2	TYR A		39.417	14.394	22.895 22.062	1.00 37.74
MOTA	1808	\mathbf{cz}	TYR A	528	39.695	15.468		1.00 35.36
MOTA	1809	ОН	TYR A		40.520	16.489	22.489 19.333	1.00 32.21
MOTA	1810	С	TYR A		37.066	10.113	19.333	1.00 32.21
MOTA	1811	0	TYR A		35.843	10.289 9.010	18.777	1.00 33.37
ATOM	1812	N	PRO A		37.601 39.034	8.705	18.673	1.00 29.41
MOTA	1813	CD	PRO A	529	36.809	7.939	18.160	1.00 30.81
ATOM	1814	CA	PRO A	529	37.875	6.895	17.822	1.00 30.02
ATOM	1815	CB	PRO A		39.061	7.703	17.564	1.00 29.92
ATOM	1816	CG	PRO A		35.706	7.331	19.040	1.00 33.28
ATOM	1817	C	PRO A	529	34.553	7.201	18.606	1.00 32.51
ATOM	1818 1819	N O	ASP A	530	36.066	6.953	20.272	1.00 35.37
ATOM ATOM	1820	CA	ASP A	530	35.110	6.338	21.195	1.00 35.88
MOTA	1821	CB	ASP A	530	35.831	5.563	22.293	1.00 46.50
ATOM	1822	CG	ASP A	530	36.564	4.341	21.758	1.00 58.80
ATOM	1823	OD1			36.010	3.219	21.852	1.00 64.43
ATOM	1824	OD2			37.697	4.503	21.240	1.00 63.77
MOTA	1825	C	ASP A		34.127	7.309	21.799	1.00 29.27
ATOM	1826	ō	ASP A		33.037	6.909	22.221	1.00 29.58
ATOM	1827	N	ILE A	531	34.525	8.577	21.892	1.00 30.58
ATOM	1828	CA	ILE A	531	33.629	9.593	22.426	1.00 29.77
ATOM	1829	CB	ILE A	531	34.302	10.998	22.576	1.00 35.01
ATOM	1830	CG2	ILE A	531	33.230	12.090	22.817	1.00 33.87
ATOM	1831	CG1	ILE A	531	35.247	10.998	23.781	1.00 36.43
ATOM	1832	CD1	ILE A	531	34.549	10.604	25.107	1.00 36.43
ATOM	1833	С	ILE A	531	32.500	9.673	21.440	1.00 29.02
MOTA	1834	0	ILE A		31.344	9.560	21.819	1.00 33.33
ATOM	1835	N	VAL A		32.841	9.787	20.158	1.00 29.79
MOTA	1836	CA	VAL A		31.814	9.857	19.129	1.00 25.98 1.00 27.17
MOTA	1837	CB	VAL A		32.446	10.141	17.746	1.00 27.17
MOTA	1838	CG1			31.376	10.244	16.699 17.788	1.00 28.57
MOTA	1839	CG2			33.246	11.437		1.00 23.34
MOTA	1840	C	VAL A		30.984	8.567	19.111 19.258	1.00 22.88
ATOM	1841	0	VAL A		29.765	8.596 7.429	19.256	1.00 23.44
MOTA	1842	N	ARG A	533 533	31.662 30.980	6.136	18.997	1.00 23.99
ATOM	1843	CA	ARG A		30.980	5.030	18.941	1.00 28.41
ATOM	1844	CB	ARG A		31.444	3.657	18.777	1.00 37.43
MOTA	1845	CG	ARG A	555	J	2.037		

							4 00	45 20
ATOM	1846	CD ARG A	533	32.551	2.627	18.668	1.00	
ATOM	1847	NE ARG A		32.255	1.490	19.528		51.73
	1848	CZ ARG A	533	32.897	1.228	20.658		55.49
ATOM		NH1 ARG A	533	33.899	2.010	21.052	1.00	51.92
MOTA	1849	MUI WEG Y	533	32.459	0.254	21.445	1.00	59.77
MOTA	1850	NH2 ARG A	. 555		5.861	20.136		24.93
MOTA	1851	C ARG A		30.024	-	19.935		24.06
MOTA	1852	O ARG A	. 533	28.866	5.504		1.00	30.94
MOTA	1853	N LEU A	534	30.519	6.093	21.348		
ATOM	1854	CA LEU A	534	29.778	5.846	22.582		26.49
	1855	CB LEU A	534	30.773	5.408	23.658		28.50
MOTA	1856	CG LEU A	534	31.461	4.072	23.339		28.71
MOTA		CD1 LEU A	534	32.692	3.806	24.193	1.00	29.88
MOTA	1857	CDI PEO N	E24	30.436	2.985	23.497	1.00	29.34
ATOM	1858	CD2 LEU A	534	28.877	6.956	23.118		24.89
MOTA	1859	C LEU A	534			23.649	1.00	
ATOM	1860	O LEU A	534	27.803	6.669			25.63
ATOM	1861	N HIS A	535	29.234	8.214	22.875		
ATOM	1862	CA HIS A	535	28.458	9.317	23.439	1.00	27.16
ATOM	1863	CB HIS A	535	29.358	10.074	24.423		26.58
ATOM	1864	CG HIS A	535	30.001	9.174	25.430		25.50
	1865	CD2 HIS A	535	31.245	8.641	25.487	1.00	25.11
ATOM		ND1 HIS A	535	29.302	8.631	26.487	1.00	26.41
MOTA	1866	CE1 HIS A	535	30.086	7.802	27.151	1.00	24.19
MOTA	1867	CEI UIS E	1 JJJ	31.270	7.790	26.564	1.00	26.77
MOTA	1868	NE2 HIS A	7 222	27.669	10.284	22.553		28.58
MOTA	1869	C HIS A	3 535	26.881	11.073	23.082		27.81
MOTA	1870	O HIS A	1 535			21.226		33.00
MOTA	1871	N PHE A	A 536	27.851	10.228			31.11
MOTA	1872	CA PHE A	¥ 536	27.092	11.108	20.313		
ATOM	1873	CB PHE A	A 536	27.895	11.401	19.043		29.90
ATOM	1874	CG PHE A	A 536	28.915	12.512	19.192		29.99
ATOM	1875	CD1 PHE A	A 536	29.678	12.643	20.337		24.61
ATOM	1876	CD2 PHE 2	A 536	29.132	13.406	18.153		25.96
	1877	CE1 PHE	A 536	30.644	13.642	20.439		23.54
MOTA	1878	CE2 PHE	A 536	30.095	14.406	18.256	1.00	24.50
MOTA		CZ PHE	A 536	30.849	14.523	19.394	1.00	24.21
MOTA	1879		A 536	25.713	10.487	19.970	100	31.08
ATOM	1880	C PHE	A 536	25.581	9.259	19.956		34.36
MOTA	1881	O PHE	A 536	24.664	11.321	19.756		27.00
MOTA	1882		A 537	24.632	12.793	19.845		25.60
MOTA	1883		A 537			19.432	1 00	25.30
MOTA	1884		A 537	23.335	10.795	19.256		23.10
MOTA	1885	CB PRO	A 537	22.501	12.068			22.43
MOTA	1886	CG PRO	A 537	23.189	13.062	20.157		30.48
MOTA	1887	C PRO	A 537	23.392	9.975	18.128		
ATOM	1888	O PRO	A 537	24.122	10.336	17.185		28.64
ATOM	1889	N PRO	A 538	22.690	8.823	18.091		31.20
ATOM	1890	CD PRO	A 538	22.017	8.173	19.227		28.91
ATOM	1891		A 538	22.654	7.946	16.908		32.16
ATOM	1892	CB PRO	A 538	21.592	6.931	17.293		29.35
MOTA	1893		A 538	21.911	6.731	18.759	1.00	28.32
	1894	C PRO	A 538	22.311	8.708	15.623		32.64
MOTA	1895	O PRO	A 538	23.086	8.680	14.669	1.00	30.42
ATOM			A 539	21.207	9.460	15.652	1.00	34.18
ATOM	1896	N LEU	A 539	20.773	10.273	14.510		30.02
MOTA	1897	CA LEU	A 222	19.512	11.069	14.895		29.47
MOTA	1898		A 539		11.924	13.802		29.66
MOTA	1899	CG LEU	A 539	18.858		12.608		31.73
MOTA	1900	CD1 LEU	A 539	18.592	11.029			25.29
MOTA	1901	CD2 LEU	A 539	17.583	12.604	14.267		
MOTA	1902	C LEU	A 539	21.887	11.215	14.009	1.00	29.19
ATOM	1903	O LEU	A 539	22.131	11.326	12.816		30.25
ATOM	1904	N TYR	A 540	22.581	11.877	14.925	1.00	25.32
ATOM	1905		A 540	23.643	12.778	14.546	1.00	22.42
ATOM	1906		A 540	24.280	13.355	15.791		21.19
ATOM	1907	CG TYR	A 540	25.343	14.387	15.535		17.26
	1908		A 540	25.016	15.733	15.400		17.30
ATOM	1909	CE1 TYR	A 540	25.982	16.676	15.216	1.00	12.79
ATOM			A 540	26.680	14.028	15.464	1.00	19.93
ATOM	1910		A 540	27.657	14.976	15.268		20.13
MOTA	1911	CEZ TIR	Y 240	27.037	14.7.0			-

WO 03/093312 PCT/EP03/04433

N COM	1912	CZ	TYR A	540	27.294	16.299	15.150	1.00	
ATOM ATOM	1913	ОН	TYR A		28.276	17.244	14.997		21.75
ATOM	1914	C	TYR A		24.708	12.009	13.780		32.70
ATOM	1915	ŏ	TYR A		25.296	12.508	12.811		34.57
ATOM	1916	N	LYS A		25.008	10.802	14.244		35.66
ATOM	1917	CA	LYS A	541	26.029	9.999	13.574		36.65
ATOM	1918	CB	LYS A		26.482	8.874	14.497		32.71
ATOM	1919	CG	LYS A		27.219	9.383	15.714		31.67
ATOM	1920	CD	LYS A		27.712	8.227	16.528	1.00	
ATOM	1921	CE	LYS A		26.561	7.418	17.035	1.00	
MOTA	1922	NZ	LYS A		27.091	6.148	17.574	1.00	
ATOM	1923	C	LYS A		25.563	9.467	12.204	_	32.35
ATOM	1924	ŏ	LYS A		26.324	9.441	11.250		34.75
ATOM	1925	Ŋ	GLU A		24.298	9.069	12.126	1.00	32.04
ATOM	1926	CA	GLU A		23.726	8.570	10.888	1.00	35.69
ATOM	1927	CB	GLU A		22.316	8.074	11.129	1.00	
ATOM	1928	CG	GLU A	542	22.269	6.772	11.888	1.00	
ATOM	1929	CD	GLU A	542	20.882	6.443	12.403	1.00	
ATOM	1930	OE1	GLU A	542	20.795	5.892	13.531		65.14
ATOM	1931	OE2	GLU A	542	19.889	6.732	11.684		59.01
ATOM	1932	С	GLU A	542	23.661	9.668	9.855		36.75
ATOM	1933	0	GLU A	542	23.668	9.393	8.666		39.22
ATOM	1934	N	LEU A	543	23.557	10.913	10.312		35.21
ATOM	1935	CA	LEU A		23.449	12.047	9.407		33.98
ATOM	1936	CB	LEU A	543	22.549	13.145	9.990		31.70
ATOM	1937	CG	LEU A		21.045	12.927	10.118		34.06
MOTA	1938	CD1	LEU A	543 ·	20.457	14.088	10.891		35.24 35.42
MOTA	1939		LEU A	543	20.388	12.826	8.761		32.29
MOTA	1940	С	LEU A		24.731	12.702	8.959 7.859		39.03
MOTA	1941	0	LEU A		24.776	13.231	9.762		29.28
MOTA	1942	N	PHE A		25.781	12.651	9.762		29.14
ATOM	1943	CA	PHE A		26.997	13.354 14.561	10.330		32.64
MOTA	1944	CB	PHE A		27.203	15.425	10.528		32.31
ATOM	1945	CG	PHE A	544	25.969	15.425	$\frac{10.326}{11.746}$		27.53
ATŌM	1946	CDI	PHE A	544	25.295 25.491	16.247	9.501	1 00	32.38
MOTA	1947	CD2	PHE A	544	24.165	16.239	11.943		26.56
ATOM	1948	CET	PHE A	544	24.103	17.065	9.690		29.30
ATOM	1949		PHE A	544	23.694	17.057	10.914		30.03
ATOM	1950	CZ C	PHE A		28.269	12.505	9.356	1.00	33.29
MOTA	1951 1952	0	PHE A		28.193	11.266	9.571		36.40
ATOM	1952		PHEA		29.349	13.102	9.110	1.00	34.60
ATOM ATOM	1954	01	HOH V	1	19.571	24.015	22.830	1.00	
ATOM	1955	01	HOH V	2	12.600	24.091	16.912	1.00	
ATOM	1956	01	HOH V	3	14.052	22.894	14.638	1.00	22.41
ATOM	1957	01	HOH V	_	28.663	16.841	27.507		23.15
ATOM	1958	01			26.725		26.728	1.00	24.50
ATOM	1959	01	нон V	6	18.179	21.587	21.082		24.52
ATOM	1960	01	HOH V	7	34.584	18.654	31.591		24.62
ATOM	1961	01	HOH V	8	38.207	8.705	22.227		25.07
ATOM	1962	01	HOH V	9	18.077	19.002	0.819		25.07
MOTA	1963	01	HOH V		17.420	26.679	24.799	1.00	25.52
MOTA	1964	01	HOH V	11	11.110	25.828	9.180		25.56
ATOM	1965	01	HOH V		25.371	34.354	26.992		25.89
MOTA	1966	01	нон V	13	35.321	27.213	19.620		25.99 26.14
MOTA	1967	01	HOH V		18.045	26.166	21.645		
MOTA	1968	01	HOH V		19.454	10.080	17.919	1 00	26.31 26.89
MOTA	1969	01	HOH V		37.357	26.490	13.415 18.302	1 00	27.31
MOTA	1970	01	HOH V		11.508	26.772	21.426		27.73
MOTA	1971	01	HOH V		15.147	25.780 37.545	37.765		27.84
MOTA	1972	01	HOH V		26.400 24.927	38.184	32.702		28.88
MOTA	1973	01	HOH V		24.927	18.724	7.093		29.31
ATOM	1974	01	HOH V		19.050	8.455	-3.987		29.80
MOTA	1975	01	HOH V		20.732	38.540	24.291		30.07
MOTA	1976		HOH V		14.054	28.783	15.745		31.20
ATOM	1977	01	HOH V	4	74.004	20.703			

MOTA	1978	01	HOH V	25	25.356	15.005	28.051		31.83
ATOM	1979	01	HOH V	26	33.279	26.348	25.938		32.16
ATOM	1980	01	HOH V	27	14.590	28.615	28.744		32.70
ATOM	1981	01	HOH V	28	4.102	35.198	9.164		32.70
ATOM	1982	01	HOH V	29	13.577	30.615	29.768		32.70
ATOM	1983	01	HOH V	30	28.564	37.851	14.236		32.76
ATOM	1984	01	HOH V	31	22.927	14.143	0.962		33.39
ATOM	1985	01	HOH V	32	27.550	38.081	22.254		33.51
ATOM	1986	01	HOH V	33	4.343	30.099	9.792		33.68
ATOM	1987	01	HOH V	34	13.758	27.478	19.451		33.73
ATOM	1988	01	HOH V	35	31.045	36.851	16.729		33.87
ATOM	1989	01	HOH V	36	19.213	14.762	21.135		33.94
ATOM	1990	01	HOH V	37	30.260	38.889	20.375		34.05
ATOM	1991	01	HOH V	38	21.211	20.354	29.122		34.10
ATOM	1992	01	HOH V	39	32.966	5.622	27.344		34.62
ATOM	1993	01	HOH V	40	26.116	6.668	20.629		35.56
ATOM	1994	01	HOH V	41	-1.516	28.517	7.655		35.63
ATOM	1995	01	HOH V	42	34.189	32.470	17.850		35.68
ATOM	1996	01	HOH V	43	24.220	21.292	3.001		35.74
MOTA	1997	01	HOH V	44	5.910	27.836	16.119		36.07
MOTA	1998	01	HOH V	45	26.026	15.360	5.513		36.54 36.65
ATOM	1999	01	HOH V	46	24.021	14.774	-1.204		
ATOM	2000	01	HOH V	47	20.363	26.930	31.179	1.00	36.70 36.70
ATOM	2001	01	HOH V	48	35.665	32.840	10.425		36.83
ATOM	2002	01	HOH V	49	26.360	37.660	34.946 -1.881	$1.00 \\ 1.00$	36.96
ATOM	2003	01	HOH V	50	25.128	17.207		1.00	37.03
MOTA	2004	01	HOH V	51	24.114	21.504	30.329		37.39
MOTA	2005	01	HOH V	52	15.366	43.743	10.778 15.530		37.82
ATOM	2006	01	HOH V	53	30.933	6.183	5.949		38.21
MOTA	2007	01	HOH V	54	4.304	36.868 35.710	19.412		39.01
ATOM	2008	01	HOH V	55	14.763		9.921		39.03
MOTA	2009	01	HOH V	56	1.357	20.195 23.892	19.724	1.00	39.09
MOTA	2010	01	HOH V	57	13.913	12.577	-11.744		39.57
MOTA	2011	01	HOH V	58	12.354	4.873	15.945		39.60
ATOM	2012	01	HOH V	59 60	19.367	27.044	-1.138		39.87
ATOM	2013	01	HOH V	60	28.823 24.086	5.629	14.333		39.92
MOTA	2014	01	HOH V	61	6.227	36.542	12.153		39.94
MOTA	2015	01	HOH V	62 63	25.257	19.031	30.271	1.00	
MOTA	2016	01	HOH V	6 <u>4</u>	33.091	35.051	17.676	1.00	40.07
MOTA	2017	01	HOH V	65	33.832	31.154	20.549	1.00	40.37
ATOM	2018	01 01	HOH V	66	40.477	15.296	9.510	1.00	41.20
MOTA	2019 2020	01	HOH V	67	23.525	9.325	-8.918	1.00	41.87
ATOM	2021	01	HOH V	68	18.624	25.089	-4.128	1.00	42.15
MOTA	2021	01	HOH V	69	24.673	39.002	-1.542	1.00	42.21
MOTA MOTA	2023	01	HOH V	70	25.134	15.085	2.723	1.00	42.21
ATOM	2024	01	HOH V	71	10.336	29.797	26.075	1.00	42.37
ATOM	2025	01	HOH V	72	16.798	18.655	-11.711	1.00	42.43
ATOM	2026	01	HOH V	73	-2.391	33.028	0.604		42.69
ATOM	2027	01	HOH V	74	7.033	20.764	20.270		43.01
MOTA	2028	01	HOH V	75	27.375	26.586	32.414		43.08
MOTA	2029	01	HOH V	76	24.651	12.458	27.335		43.14
ATOM	2030	01	HOH V	77	21.223	24.850	0.260		43.31
ATOM	2031	01	HOH V	78	13.059	10.272	13.532		43.63
ATOM	2032	01	V HOH	79	27.284	19.103	8.210		44.00
ATOM	2033	01	HOH V	80	34.897	34.595	21.757		44.35
ATOM	2034	01	HOH V	81	19.496	24.289	-1.468		44.41
ATOM	2035	01	HOH V	82	26.589	22.429	32.257		44.58
MOTA	2036	01	HOH V	83	41.875	11.753	22.776		44.72
MOTA	2037	01	HOH V	84	24.041	16.824	29.300	1.00	44.91 45.03
ATOM	2038	01	HOH V	85	39.182	23.600	24.591		45.03
ATOM	2039	01	HOH V	86	16.711	29.367	31.469	1.00	45.42
ATOM	2040	01	HOH V	87	26.474	37.247	27.330 7.001	1 00	45.46
MOTA	2041	01	HOH V		10.580	10.952	23.482	1 00	45.53
ATOM	2042	01			17.919	17.134	33.013	1 00	45.86
MOTA	2043	01	HOH V	90	22.700	27.169	33.013		10.00

								4 00 46 30
ATOM	2044	01	HOH V 91		218	40.609	29.025	1.00 46.30
ATOM	2045	01	HOH V 92		955	40.569	26.103	1.00 46.31
ATOM	2046	01	HOH V 93		333	26.234	18.852	1.00 46.91
ATOM	2047	01	HOH V 94	6.	403	18.038	15.920	1.00 47.12
ATOM	2048	01	HOH V 95	37.	307	11.015	10.807	1.00 47.31
ATOM	2049	01	HOH V 96		338	13.464	13.985	1.00 47.96
ATOM	2050	01	HOH V 97	10.	441	37.707	30.346	1.00 48.02
ATOM	2051	01	HOH V 98	30.	888	36.428	14.084	1.00 48.48
	2052	01	HOH V 99		882	17.980	29.841	1.00 48.50
MOTA	2053	01	HOH V 100		749	37.917	8.734	1.00 48.51
MOTA	2054	01	HOH V 101		379	27.870	33.046	1.00 48.64
MOTA	2055	01	HOH V 102		449	31.668	8.141	1.00 48.94
ATOM	2056	01	HOH V 103		164	17.601	3.576	1.00 49.29
ATOM	2057	01	HOH V 104		653	32.899	6.888	1.00 49.36
MOTA	2058	01	HOH V 105		507	15.827	13.475	1.00 49.69
MOTA	2059	01	HOH V 106		222	20.712	33.061	1.00 49.71
ATOM	2060	01	HOH V 107	19	173	42.140	26.556	1.00 49.87
MOTA		01	HOH V 108		128	28.133	10.338	1.00 50.07
MOTA	2061	01	HOH V 109		605	40.750	25.634	1.00 50.16
ATOM	2062	01	HOH V 110		. 457	28.059	-4.001	1.00 50.19
ATOM	2063	01	HOH V 111		.092	31.118	6.416	1.00 50.25
ATOM	2064	01	HOH V 112		.374	39.612	-3.935	1.00 50.31
ATOM	2065	01	HOH V 112		.127	18.267	32.763	1.00 50.37
ATOM	2066	01	HOH V 114		.258	23.101	26.041	1.00 50.51
ATOM	2067	01	HOH V 115		.516	26.089	-3.694	1.00 50.63
MOTA	2068	01	HOH V 115		.352	17.048	19.784	1.00 50.83
MOTA	2069 2070	01	HOH V 117		. 647	6.108	12.167	1.00 50.93
ATOM	2070	01	HOH V 118		.146	17.547	1.891	1.00 50.94
ATOM	2072	01	HOH V 119		.203	21.870	20.133	1.00 50.98
ATOM ATOM	2073	01	HOH V 120	32	.029	18.786	4.116	1.00 51.10
ATOM	2074	01	HOH V 121	22	.114	18.269	27.109	1.00 51.46
MOTA	2075	01	HOH V 122	25	. 668	18,396	5.657	1.00 51.52
ATOM	2076	01	HOH V 123		.989	18.102	20.145	1.00 51.77
ATOM	2077	01	HOH V 124		.078	5.753	14.297	1.00 52.16
ATOM	2078	01	HOH V 125		. 191	23,385	-0.546	1.00 52.19
ATOM	2079	01	HOH V 126		.840	23.465	28.263	1.00 52.44
ATOM	2080	01	HOH V 127		.889	40.107	16.024	1.00 52.46 1.00 52.47
MOTA	2081	01	HOH V 128		.480	31.213	29.646	1.00 52.47
MOTA	2082	01	HOH V 129		.041	40.539	4.064 30.124	1.00 52.65
ATOM	2083	01	HOH V 130	25	.662	37.407 19.513	14.379	1.00 52.05
MOTA	2084	01	HOH V 131			36.654	28.009	1.00 52.82
ATOM	2085	01	HOH V 132		.355	25.685	32.162	1.00 52.92
ATOM	2086	01	HOH V 133 HOH V 134		.710	0.923	19.113	1.00 52.92
MOTA	2087	01	HOH V 134		.608	9.016	9.185	1.00 52.96
MOTA	2088	01 01	HOH V 136		.883	4.742	16.973	1.00 53.32
MOTA	2089 2090	01	HOH V 137		.325	41.144	15.563	1.00 54.00
MOTA	2091	01	HOH V 138		.148	32.691	27.089	1.00 54.14
ATOM ATOM	2092	01	HOH V 139		.869	44.302	17.088	1.00 54.60
ATOM	2093	01	HOH V 140		.180	24.098	0.471	1.00 54.96
ATOM	2094	01	HOH V 141	32	.092	39.604	16.380	1.00 55.48
MOTA	2095	01	HOH V 142	20	.031	28.982	35.641	1.00 55.95
MOTA	2096	01	HOH V 143		.537	17.716	26.209	1.00 56.58
MOTA	2097	01	HOH V 144	3	.004	26.615	21.765	1.00 56.65
ATOM	2098	01	HOH V 145		.566	13.601	10.033	1.00 56.98
ATOM	2099	01	HOH V 146		.090	48.803	-0.839	1.00 57.02
MOTA	2100	01	HOH V 147		521	30.957	16.321	1.00 57.24
ATOM	2101	01	HOH V 148		322	6.331	6.002	1.00 57.58
ATOM	2102	01	HOH V 149		375	39.538	12.218	1.00 57.59
ATOM	2103	01	HOH V 150		176	39.661	18.686	1.00 58.07 1.00 58.21
MOTA	2104	01	HOH V 151		363	24.179	31.362	1.00 58.21
ATOM	2105	01			1.157	40.583	21.313	1.00 58.51
ATOM	2106	01	HOH V 153		3.420	36.512	16.363 4.549	1.00 58.55
MOTA	2107	01			L.911 5.108	36.126 6.884	12.075	1.00 58.70
MOTA	2108	01			1.815	29.631	-4.704	1.00 58.74
MOTA	2109	01	HOH A TOO		UJ			

- 64 -

				17.728	4.118	0.882	1.00	59.17
ATOM	2110	01	HOH V 157			31.437	1.00	
ATOM	2111	01	HOH V 158	11.034	33.423	9.565	1.00	
ATOM	2112	01	HOH V 159	39.277	19.752			59.89
ATOM	2113	01	HOH V 160	20.830	23.224	-9.945		
ATOM	2114	01	HOH V 161	29.709	18.612	31.510	1.00	
ATOM	2115	01	HOH V 162	27.074	2.621	20.642		60.12
ATOM	2116	01	HOH V 163	5.858	22.161	-4.489	1.00	
	2117	01	HOH V 164	15.034	44.034	5.590	1.00	60.39
MOTA			HOH V 165	33.009	22.978	33.387	1.00	60.43
MOTA	2118	01	HOH V 165	2.030	21.719	-4.397	1.00	
MOTA	2119	01	HOH V 166	3.774	21.532	3.731		60.68
MOTA	2120	01	HOH V 167	28.412	13.665	-7.177	1.00	
MOTA	2121	01	HOH V 168		22.162	31.337		61.22
ATOM	2122	01	HOH V 169	39.061		11.347		61.45
ATOM	2123	01	HOH V 170	30.385	11.086			61.62
MOTA	2124	01	HOH V 171	38.929	11.728	26.423		
MOTA	2125	01	HOH V 172	9.596	6.343	-6.409		61.85
ATOM	2126	01	HOH V 173	27.960	21.516	2.108		61.90
ATOM	2127	01	HOH V 174	4.313	13.515	-0.097		62.15
ATOM	2128	01	HOH V 175	-4.186	27.811	7.260		62.60
	2129	01	HOH V 176	10.940	41.489	27.508		63.29
ATOM	2130	01	HOH V 177	24.701	19.822	-1.623		63.64
ATOM		01	HOH V 178	42.644	18.535	10.330	1.00	63.68
ATOM	2131		HOH V 179	1.986	36.706	26.540	1.00	63.68
MOTA	2132	01	HOH V 179	22.345	47.189	18.548		64.72
MOTA	2133	01	HOH V 180	7.492	6.994	1.249		64.77
MOTA	2134	01	HOH V 181		37.819	26.783		64.90
MOTA	2135	01	HOH V 182	29.348		25.832		65.05
MOTA	2136	01	HOH V 183	39.883	20.258			65.28
MOTA	2137	01	HOH V 184	33.197	24.977	3.656		65.41
ATOM	2138	01	HOH V 185	1.167		3.205		65.48
ATOM	2139	01	HOH V 186	36.275	32.735	23.649		
ATOM	2140	01	HOH V 187	-2.787	30.904	-0.828	1.00	65.58
ATOM	2141	01	HOH V 188	6.538		-10.695		66.34
ATOM	2142	01	HOH V 189	10.682	8.724	11.380		66.87
ATOM	2143	01	HOH V 190	14.198	8.869	-12.442		67.21
ATOM	2144	01	HOH V 191	-2.267	38.672	-2.479		67.22
	2145	01	HOH V 192	29.224	8.950	12.107	1.00	67.30
MOTA	2145	01	HOH V 193	11.819	8.883	6.281	1.00	67.62
MOTA		01	HOH V 194	38.489	16.915	8.462	1.00	68.36
MOTA	2147		HOH V 195	33.987	7.482	15.967	1.00	68.84
ATOM	2148	01	HOH V 196	4.892	34.328	-7.351		68.88
MOTA	2149	01	HOH V 190	39.056	27.510	8.823	1.00	68.92
ATOM	2150	01	HOH V 197	9.884	6.802	3.712		69.08
MOTA	2151	01	HOH V 198	37.843	34.495	12.256		69.20
MOTA	2152	01	HOH V 199		36.343	19.667		69.76
ATOM	2153	01	HOH V 200	34.349		20.411		70.03
ATOM	2154	01	HOH V 201	38.474	1.028		1.00	
MOTA	2155	01	HOH V 202	27.053	38.768	25.134		70.65
ATOM	2156	01	HOH V 203	28.267	37.799	29.494		
ATOM	2157	01	HOH V 204	25.427		1.054		71.85
ATOM	2158	01	HOH V 205	18.375	3.341	9.734		72.08
ATOM	2159	01	HOH V 206	29.055	24.527	-1.260	1.00	
ATOM	2160	01	HOH V 207	15.436	3.667	-5.477	1.00	
ATOM	2161	01	HOH V 208	2.845	25.343	17.594	1.00	72.71
ATOM	2162	01	HOH V 209	31.127	39.615	33.793	1.00	74.83
	2163	01	HOH V 210	15.559	12.402	-12.936	1.00	75.70
MOTA			HOH V 211	40.158	26.133	22.103	1.00	76.15
ATOM	2164	01	HOH V 212	3.811	32.891	15.563	1.00	77.51
MOTA	2165	01	TOT V 212	21.251	45.356	7.011	1.00	
ATOM	2166	01	HOH V 213	31.582	39.863	24.269	1.00	
ATOM	2167	01	HOH V 214	-0.088	20.677	7.373	1.00	79.61
ATOM	2168	01	HOH V 215	34.466	33.712	35.188		80.04
ATOM	2169	01	HOH V 216			2.187	1 00	82.20
MOTA	2170	01	HOH V 217	5.299	14.605			82.43
MOTA	2171	01	HOH V 218	-0.119	43.183	-1.190		83.22
MOTA	2172	01	HOH V 219	21.612	10.359			83.87
ATOM	2173	01	HOH V 220	18.145	42.688	23.379	1.00	03.07
ATOM	2174	01	HOH V 221	38.141	26.882	26.796	1.00	84.27
ATOM	2175	01	HOH V 222	15.645	37.869	15.459	T.00	86.80

	TOM	2176	01	нон			33.347 26.717	0.052 9.812	24.088 6.181		88.51 89.08
A	MOT	2177	01	нон				7.603	15.584		89.47
Α	MOT	2178	01	HOH			13.496	31.611	9.140		89.58
A	MOT	2179	01	HOH			0.897	26.525	-7.628		90.92
A	MOT	2180	01	HOH	V	227	13.018		17.755		91.50
A	MOT	2181	01	HOH	V	228	6.286	19.849	0.669		92.59
A	MOT	2182	01	HOH			19.825	7.712	20.218		93.48
A	MOT	2183	01	HOH			16.141	11.181	18.146	1.00	94.31
	MOT	2184	01	нон			30.341	41.381	16.146	1.00	17.77
P	MOT	2185	C1	CHO		1	18.565	26.648		1.00	14.30
P	MOT	2186	C4	CHO		1	17.062	26.995	16.208	1.00	16.71
F	MOTA	2187	C7	CHO		1	16.300	25.791	16.806	1.00	17.53
7	MOTA	2188	C9	CHO		1	16.836	25.493	18.221	1.00	21.09
7	MOTA	2189	C12	CHO		1	18.329	25.274	18.190	1.00	17.61
7	MOTA	2190	C13	CHO		1	18.814	24.179	18.791	1.00	16.99
7	MOTA	2191	C15		_	1	20.283	23.851	18.848	1.00	18.07
7	MOTA	2192		CHO		1	21.159	25.087	18.576	1.00	18.92
7	MOTA	2193		CHO		1	20.643	25.806	17.292	1.00	20.91
7	MOTA	2194	C22			1	19.182	26.326	17.485	1.00	19.33
7	MOTA	2195	C23	CHO		1	21.613	26.937	16.851 16.727	1.00	23.26
	MOTA	2196	C26	CHO		1	23.077	26.440		1.00	24.98
7	MOTA	2197	C29	CHO		1	23.552	25.816	18.063	1.00	19.40
7	MOTA	2198	C30	CHO	L	1	22.616	24.628	18.351	1.00	18.81
1	MOTA	2199	C32	CHO		1	23.316	23.866	19.486	1.00	18.34
1	MOTA	2200	C35			1	24.818	24.074	19.179	1.00	20.78
	MOTA	2201		CHO		1	24.905	25.059	17.980	1.00	25.58
	MOTA	2202		CHO		1	23.518	26.864	19.214	1.00	21.74
	MOTA	2203		CHO			19.179	27.650	18.304	1.00	18.44
	MOTA	2204		CHO			26.193	25.932	18.008	1.00	20.10
	MOTA	2205		CHO			26.277	26.915	16.822	1.00	18.74
	MOTA	2206	C54	CHO	L		27.502	25.106	18.059	1.00	19.99
	MOTA	2207	C57				27.623	23.980	17.005	1.00	
	ATOM	2208	C60	CHO	L		29.075	23.453	17.059	1.00	
	MOTA	2209	C63	CHO	L		29.308	22.160	16.245	1.00	
	ATOM	2210	C65	CHO	L		30.827	21.916	16.132		
	MOTA	2211	C69	CHO	L		28.658	20.944	16.934	1.00	
	ATOM	2212	073	CHO	L	. 1	14.905	26.073	16.943	1.00	44.11
	END										

7	r_{\sim}	ы	•	O
	a	IJ	c	"

ATOM 1 N	Labics									co oo
ATOM 2 CA HIS A 261 -17.481 28.056 -11.002 1.00 ATOM 4 CG HIS A 261 -18.304 27.204 -11.961 1.00 ATOM 5 ND1 HIS A 261 -17.529 26.743 -13.153 1.00 ATOM 6 CE1 HIS A 261 -17.529 26.743 -13.153 1.00 ATOM 7 NE2 HIS A 261 -16.705 26.824 -15.195 1.00 ATOM 8 CD2 HIS A 261 -16.705 26.824 -15.195 1.00 ATOM 9 C HIS A 261 -16.754 25.650 -13.342 1.00 ATOM 10 O HIS A 261 -16.754 25.650 -13.342 1.00 ATOM 10 O HIS A 261 -15.409 29.012 -11.759 1.00 ATOM 11 N HIS A 262 -17.695 31.652 -14.199 1.00 ATOM 12 CA HIS A 262 -17.695 31.652 -14.199 1.00 ATOM 13 CB HIS A 262 -17.695 31.652 -14.199 1.00 ATOM 15 ND1 HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 16 CE1 HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 17 NE2 HIS A 262 -18.957 29.586 -16.959 1.00 ATOM 18 CD2 HIS A 262 -18.957 29.586 -16.959 1.00 ATOM 19 C HIS A 262 -18.967 29.586 -16.291 3.00 ATOM 19 C HIS A 262 -18.967 29.586 -16.291 3.00 ATOM 19 C HIS A 262 -18.967 29.586 -16.291 3.00 ATOM 20 O HIS A 262 -15.815 31.792 -12.437 1.00 ATOM 21 N LEU A 263 -16.300 32.109 -11.235 1.00 ATOM 22 CA LEU A 263 -16.300 32.109 -11.235 1.00 ATOM 23 CB LEU A 263 -16.300 32.109 -11.235 1.00 ATOM 24 CG LEU A 263 -15.815 31.792 -12.810 1.00 ATOM 26 CD1 LEU A 263 -15.815 31.792 -12.810 1.00 ATOM 27 C LEU A 263 -15.844 32.829 -10.282 1.00 ATOM 28 O LEU A 263 -15.844 32.289 -10.282 1.00 ATOM 29 N GLU A 264 -14.997 30.672 -9.638 1.0 ATOM 26 CD2 LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 30 CA GLU A 264 -14.297 30.672 -9.638 1.0 ATOM 31 CB GLU A 264 -14.293 29.797 -1.516 1.0 ATOM 32 CD GLU A 264 -14.293 29.799 -1.01.281 1.00 ATOM 34 CD1 LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 36 C GLU A 264 -14.800 25.693 -7.476 1.0 ATOM 37 C GLU A 264 -14.800 25.693 -7.476 1.0 ATOM 38 N VAL A 265 -11.792 29.797 -1.516 1.0 ATOM 39 CA GLU A 264 -14.800 25.693 -7.476 1.0 ATOM 30 CA GLU A 264 -14.800 25.693 -7.476 1.0 ATOM 31 CB GLU A 264 -14.800 25.693 -7.476 1.0 ATOM 32 CD LEU A 266 -1.348 30.999 -1.0.251 1.0 ATOM 36 C GLU A 264 -14.800 25.693 -7.476 1.0 ATOM 37 C LEU A 266 -1.348 30.999 -1.0.251 1.0 ATOM 40 CB VAL A 265 -1	ATOM						28.759	-10.025	1.00	
ATOM 5 NIN HIS A 261 -17.529 26.743 -13.153 1.00 ATOM 5 NIN HIS A 261 -16.705 26.824 -15.195 1.00 ATOM 7 NEZ HIS A 261 -16.705 26.824 -15.195 1.00 ATOM 7 NEZ HIS A 261 -16.754 25.650 -13.342 1.00 ATOM 9 C HIS A 261 -16.754 25.650 -13.342 1.00 ATOM 9 C HIS A 261 -16.640 29.033 -11.812 1.00 ATOM 10 O HIS A 261 -15.409 29.012 -11.759 1.00 ATOM 11 N HIS A 262 -17.309 29.814 -12.647 1.00 ATOM 12 CA HIS A 262 -17.309 29.814 -12.647 1.00 ATOM 13 CB HIS A 262 -17.695 31.652 -14.199 1.00 ATOM 14 CG HIS A 262 -17.695 31.652 -14.199 1.00 ATOM 15 NDI HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 16 CEI HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 17 NEZ HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 18 CDZ HIS A 262 -18.862 30.538 -16.516 -10.00 ATOM 19 C HIS A 262 -18.862 30.538 -16.516 -10.00 ATOM 20 O HIS A 262 -14.698 32.162 -12.810 1.00 ATOM 20 O HIS A 262 -14.698 32.162 -12.810 1.00 ATOM 20 O HIS A 263 -15.849 32.829 -10.282 1.00 ATOM 21 N LEU A 263 -15.449 32.829 -10.282 1.00 ATOM 22 CA LEU A 263 -15.449 32.829 -10.282 1.00 ATOM 24 CG LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 25 CDD LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 26 CDZ LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 27 C LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 28 O LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 29 N GLU A 264 -13.359 -9.9682 1.00 ATOM 31 CB GLU A 264 -14.421 31.965 -9.840 1.00 ATOM 32 CB LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 33 CD GLU A 264 -13.497 30.672 -9.682 1.00 ATOM 34 CEI GLU A 264 -14.497 30.672 -9.682 1.00 ATOM 35 CE CDZ LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 36 C CDZ LEU A 265 -17.692 34.934 -7.824 1.00 ATOM 37 CB LEU A 266 -17.693 31.354 -9.920 1.00 ATOM 38 N VAL A 265 -17.693 30.999 -10.255 -0.00 ATOM 39 CA LEU A 266 -17.693 30.999 -10.255 -0.00 ATOM 30 CA GLU A 264 -13.497 30.672 -9.638 1.00 ATOM 30 CA GLU A 264 -13.497 30.672 -9.682 1.00 ATOM 31 CB GLU A 264 -13.497 30.672 -9.692 1.00 ATOM 32 CB LEU A 265 -17.695 30.999 -10.251 1.00 ATOM 36 CB LEU A 266 -17.699 30.999 -10.251 1.00 ATOM 37 CB LEU A 266 -17.498 34.492 -17.402 -9.638 1.0			CA I	HIS A	261		28.056	-II.UUZ	-	61.45
ATOM ATOM ATOM ATOM ATOM ATOM ATOM ATOM			CB I	HIS A	261					63.15
ATOM 5 NDI HIS A 261	MOTA		CG	HIS A	261					65.59
ATOM 7 NE2 HIS A 261 -16.255 25.723 -14.620 1.00 ATOM 8 CD2 HIS A 261 -16.640 29.033 -11.812 1.00 ATOM 10 0 HIS A 261 -16.640 29.033 -11.812 1.00 ATOM 11 N HIS A 262 -16.661 30.904 -13.361 1.00 ATOM 12 CA HIS A 262 -16.661 30.904 -13.361 1.00 ATOM 13 CB HIS A 262 -16.661 30.904 -13.361 1.00 ATOM 14 CG HIS A 262 -17.695 31.652 -14.199 1.00 ATOM 15 ND1 HIS A 262 -17.695 31.652 -14.199 1.00 ATOM 16 CE1 HIS A 262 -19.744 29.220 -15.954 1.00 ATOM 17 NE2 HIS A 262 -19.744 29.220 -15.954 1.00 ATOM 17 NE2 HIS A 262 -18.082 30.538 -16.516 1.00 ATOM 18 CD2 HIS A 262 -18.082 30.538 -16.516 1.00 ATOM 19 C HIS A 262 -15.815 31.792 -12.437 1.00 ATOM 20 O HIS A 262 -15.815 31.792 -12.437 1.00 ATOM 21 N LEU A 263 -16.300 32.109 -11.235 1.00 ATOM 22 CA LEU A 263 -16.300 32.109 -11.235 1.00 ATOM 23 CB LEU A 263 -16.202 33.286 -9.044 1.00 ATOM 24 CG LEU A 263 -16.866 34.666 -9.101 1.00 ATOM 25 CD1 LEU A 263 -15.849 32.829 -10.282 1.00 ATOM 26 CD2 LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 27 C LEU A 263 -15.841 31.965 -9.840 1.00 ATOM 28 O LEU A 263 -15.841 32.463 -9.682 1.00 ATOM 29 N GLU A 264 -14.497 30.6772 -9.688 1.00 ATOM 30 CA GLU A 264 -14.497 30.6772 -9.688 1.00 ATOM 31 CB GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 32 CG GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 33 CD GLU A 264 -14.497 30.6772 -9.688 1.00 ATOM 34 OE1 GLU A 264 -14.497 30.6772 -9.688 1.00 ATOM 35 OE2 GLU A 264 -12.339 29.599 -13.923 1.00 ATOM 36 C GLU A 264 -14.497 30.6772 -9.688 1.00 ATOM 37 O GLU A 264 -12.339 29.599 -13.923 1.00 ATOM 38 N VAL A 265 -11.722 29.766 -12.574 1.00 ATOM 39 CA VAL A 265 -11.436 32.463 -9.244 1.00 ATOM 30 CE GLU A 264 -14.497 30.6772 -9.688 1.00 ATOM 37 O GLU A 264 -14.800 25.693 -7.476 1.00 ATOM 38 N VAL A 265 -11.722 29.766 -12.574 1.00 ATOM 39 CA VAL A 265 -11.722 39.756 -19.251 1.00 ATOM 40 CB VAL A 266 -11.655 35.012 -14.004 1.00 ATOM 50 CE UAL A 266 -11.497 30.994 -19.251 1.00 ATOM 50 CD2 LEU A 266 -11.497 30.994 -19.251 1.00 ATOM 50 CD2 LEU A 266 -11.605 36.617 -6.969 1.00 ATOM 50 CD2 LEU A 266 -10.780 34.497 -9.397 11.00		5	NDT I	HID A	261		26.824	-15.195	1.00	
ATOM		5	MES I	HTO Y	261				1.00	
ATOM 9 C HIS A 261 -16.640 29.033 -11.812 1.00 ATOM 10 O HIS A 262 -17.309 29.012 -11.759 1.00 ATOM 11 N HIS A 262 -17.309 29.012 -11.759 1.00 ATOM 12 CA HIS A 262 -17.309 29.814 -12.647 1.00 ATOM 12 CA HIS A 262 -16.661 30.904 -13.361 1.00 ATOM 13 CB HIS A 262 -18.358 30.763 -15.209 1.00 ATOM 14 CG HIS A 262 -18.358 30.763 -15.209 1.00 ATOM 15 NDII HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 16 CE1 HIS A 262 -19.744 29.220 -15.954 1.00 ATOM 17 NE2 HIS A 262 -19.744 29.220 -15.954 1.00 ATOM 18 CD2 HIS A 262 -18.967 29.586 -16.555 1.00 ATOM 19 C HIS A 262 -18.082 30.538 -16.516 1.00 ATOM 20 O HIS A 262 -18.082 30.538 -16.516 1.00 ATOM 21 N LEU A 263 -16.803 32.162 -12.810 1.00 ATOM 22 CA LEU A 263 -15.449 32.829 -10.282 1.00 ATOM 23 CB LEU A 263 -15.449 32.829 -10.282 1.00 ATOM 24 CG LEU A 263 -15.841 32.829 -10.282 1.00 ATOM 25 CD1 LEU A 263 -15.841 31.956 -9.044 1.00 ATOM 26 CD2 LEU A 263 -15.841 31.956 -9.840 1.00 ATOM 27 C LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 28 O LEU A 263 -15.841 31.956 -9.840 1.00 ATOM 29 N GLU A 264 -13.154 32.463 -9.682 1.00 ATOM 30 CA GLU A 264 -13.450 29.748 -9.682 1.00 ATOM 31 CB GLU A 264 -13.227 27.462 -8.006 1.00 ATOM 32 CG GLU A 264 -13.227 27.462 -8.006 1.00 ATOM 33 CD GLU A 264 -14.800 25.693 -7.476 1.00 ATOM 34 OE1 GLU A 264 -13.227 27.462 -8.006 1.00 ATOM 35 OE2 GLU A 264 -14.800 25.693 -7.476 1.00 ATOM 36 C GLU A 264 -12.339 29.694 -10.251 1.00 ATOM 37 O GLU A 264 -12.339 29.595 -13.923 1.00 ATOM 38 N VAL A 265 -11.780 34.586 -12.195 1.00 ATOM 39 CA VAL A 2665 -11.780 34.586 -12.195 1.00 ATOM 39 CA VAL A 2665 -11.488 32.164 -12.896 1.00 ATOM 30 CD CD2 LEU A 2664 -14.800 25.693 -7.476 1.00 ATOM 36 C GLU A 264 -13.227 27.462 -8.006 1.00 ATOM 37 O GLU A 264 -14.800 25.693 -7.476 1.00 ATOM 38 N VAL A 265 -11.780 34.586 -12.195 1.00 ATOM 39 CA VAL A 266 -10.898 31.00 34.12.599 1.00 ATOM 39 CA VAL A 266 -10.898 31.00 34.889 -13.923 1.00 ATOM 39 CA VAL A 266 -10.898 31.00 34.11.40 1.00 ATOM 39 CA VAL A 266 -10.898 31.00 34.899 -13.400 1.00 ATOM 40 CD LEU A 266 -10.898 31.00 34.		8	CD2 I	HTS A	261				1.00	
ATOM 10 O HIS A 261 -15.409 29.012 -11.759 1.07 ATOM 11 N HIS A 262 -17.309 29.814 -12.647 1.00 ATOM 12 CA HIS A 262 -16.661 30.904 -13.361 1.00 ATOM 13 CB HIS A 262 -16.661 30.904 -13.361 1.00 ATOM 14 CG HIS A 262 -16.661 30.904 -13.361 1.00 ATOM 15 ND1 HIS A 262 -18.358 30.763 -15.209 1.00 ATOM 16 CEI HIS A 262 -19.744 29.220 -15.954 1.00 ATOM 17 NE2 HIS A 262 -19.744 29.220 -15.954 1.00 ATOM 17 NE2 HIS A 262 -19.744 29.220 -15.954 1.00 ATOM 18 CD2 HIS A 262 -18.967 29.586 -16.959 1.00 ATOM 19 C HIS A 262 -18.967 29.586 -16.959 1.00 ATOM 20 O HIS A 262 -14.698 30.538 -16.516 1.00 ATOM 20 O HIS A 262 -14.698 32.162 -12.810 1.00 ATOM 21 N LEU A 263 -16.300 32.109 -11.235 1.00 ATOM 22 CA LEU A 263 -15.449 32.829 -10.282 1.00 ATOM 24 CG LEU A 263 -16.221 33.286 -9.044 1.00 ATOM 25 CD1 LEU A 263 -16.866 34.666 -9.101 1.00 ATOM 26 CD2 LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 27 C LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 28 O LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 29 N GLU A 264 -14.497 30.672 -9.682 1.00 ATOM 30 CA GLU A 264 -14.497 30.672 -9.682 1.00 ATOM 31 CB GLU A 264 -14.497 30.672 -9.688 1.00 ATOM 32 CG GLU A 264 -14.497 30.672 -9.688 1.00 ATOM 33 CD GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 34 OEI GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 35 OE2 GLU A 264 -14.393 29.694 -19.251 1.00 ATOM 36 C GLU A 264 -14.393 29.694 -19.251 1.00 ATOM 37 O GLU A 264 -12.339 29.694 -19.251 1.00 ATOM 38 N VAL A 265 -12.709 29.797 -11.556 1.00 ATOM 39 CA VAL A 265 -12.709 29.797 -11.556 1.00 ATOM 40 CB VAL A 265 -11.722 29.766 -12.574 1.00 ATOM 40 CB VAL A 266 -11.488 32.164 -12.282 1.00 ATOM 41 CGI VAL A 266 -11.488 32.164 -12.282 1.00 ATOM 45 N LEU A 266 -11.488 32.164 -12.282 1.00 ATOM 46 CA LEU A 266 -11.488 32.164 -12.282 1.00 ATOM 50 CC PHE A 267 -9.914 32.713 -10.094 1.00 ATOM 51 C LEU A 266 -11.488 32.164 -12.282 1.00 ATOM 50 CC PHE A 267 -9.935 32.758 -8.931 1.00 ATOM 50 CC PHE A 267 -9.935 32.758 -8.931 1.00 ATOM 50 CC PHE A 267 -9.945 35.138 -6.6864 1.00 ATOM 50 CC PHE A 267 -9.945 35.138 -6.864 1.00 ATOM 50 CC			C	HIS A	261	-16.640			1.00	
ATOM 11 N HIS A 262 -17.309 29.814 -12.647 1.00 ATOM 12 CA HIS A 262 -16.661 30.904 -13.361 1.00 ATOM 13 CB HIS A 262 -17.695 31.652 -14.199 1.00 ATOM 14 CG HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 15 ND1 HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 16 CE1 HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 17 NE2 HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 18 CD2 HIS A 262 -19.744 29.220 -15.954 1.00 ATOM 18 CD2 HIS A 262 -18.967 29.586 -16.959 1.00 ATOM 19 C HIS A 262 -18.967 29.586 -16.959 1.00 ATOM 20 O HIS A 262 -18.963 30.763 -16.516 1.00 ATOM 21 N LEU A 263 -16.808 32.162 -12.810 1.00 ATOM 22 CA LEU A 263 -16.49 32.209 -11.235 1.00 ATOM 23 CB LEU A 263 -16.49 32.829 -10.282 1.00 ATOM 24 CG LEU A 263 -16.866 34.666 -9.101 1.00 ATOM 25 CD1 LEU A 263 -16.866 34.666 -9.101 1.00 ATOM 26 CD2 LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 27 C LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 28 O LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 29 N GLU A 264 -14.497 30.672 -9.638 1.00 ATOM 30 CA GLU A 264 -14.497 30.672 -9.638 1.00 ATOM 31 CB GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 33 CD GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 34 OEI GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 35 OE2 GLU A 264 -13.227 27.462 -8.006 1.00 ATOM 36 C GLU A 264 -13.227 27.462 -8.006 1.00 ATOM 37 O GLU A 264 -13.227 27.462 -8.006 1.00 ATOM 38 N VAL A 265 -12.393 29.659 -13.923 1.00 ATOM 39 CA VAL A 265 -12.393 29.659 -7.476 1.00 ATOM 30 CA VAL A 266 -11.722 29.766 -12.574 1.00 ATOM 40 CB VAL A 265 -12.393 29.559 -13.3223 1.00 ATOM 40 CB VAL A 266 -11.488 32.144 -12.2896 1.00 ATOM 40 CB VAL A 266 -11.488 32.142 -11.08 1.00 ATOM 40 CB VAL A 266 -11.488 32.173 -11.140 1.00 ATOM 50 CD LEU A 266 -11.655 55.012 -14.609 1.00 ATOM 50 CD LEU A 266 -11.655 55.012 -14.609 1.00 ATOM 50 CD LEU A 266 -11.655 55.012 -14.609 1.00 ATOM 50 CD LEU A 266 -11.655 55.012 -14.609 1.00 ATOM 50 CD PHE A 267 -9.035 32.778 -8.931 1.00 ATOM 50 CD PHE A 267 -9.035 32.778 -8.931 1.00 ATOM 50 CD PHE A 267 -9.035 32.778 -8.931 1.00 ATOM 50 CD PHE A 267 -9.035 32.778 -8.931 1.00		-				-15.409			1.00	60.45
ATOM 12 CA HIS A 262 -16.661 30.904 -13.361 1.004 ATOM 13 CB HIS A 262 -17.695 31.652 -14.199 1.00 ATOM 14 CG HIS A 262 -18.358 30.763 -15.209 1.00 ATOM 15 ND1 HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 16 CE1 HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 17 NE2 HIS A 262 -19.744 29.220 -15.954 1.00 ATOM 17 NE2 HIS A 262 -18.082 30.538 -16.516 1.00 ATOM 18 CD2 HIS A 262 -18.082 30.538 -16.516 1.00 ATOM 19 C HIS A 262 -18.082 30.538 -16.516 1.00 ATOM 20 O HIS A 262 -15.815 31.792 -12.437 1.00 ATOM 21 N LEU A 263 -16.60 30 32.109 -11.235 1.00 ATOM 21 N LEU A 263 -16.300 32.109 -11.235 1.00 ATOM 22 CA LEU A 263 -16.221 33.286 -9.044 1.00 ATOM 23 CB LEU A 263 -16.221 33.286 -9.044 1.00 ATOM 24 CG LEU A 263 -16.866 34.666 -9.101 1.00 ATOM 25 CD1 LEU A 263 -16.866 34.666 -9.101 1.00 ATOM 26 CD2 LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 27 C LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 29 N GLU A 264 -13.450 29.748 -9.682 1.00 ATOM 29 N GLU A 264 -13.450 29.748 -9.682 1.00 ATOM 30 CA GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 31 CB GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 33 CD GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 34 OE1 GLU A 264 -13.350 29.748 -9.204 1.00 ATOM 35 OE2 GLU A 264 -13.350 29.748 -9.204 1.00 ATOM 36 C GLU A 264 -13.227 27.462 -8.006 1.00 ATOM 37 O GLU A 264 -13.297 27.462 -8.006 1.00 ATOM 38 N VAL A 265 -12.393 29.599 -9.920 1.00 ATOM 36 C GLU A 264 -12.339 29.599 -9.920 1.00 ATOM 37 O GLU A 264 -12.339 29.599 -10.225 1.00 ATOM 38 N VAL A 265 -12.709 29.797 -11.551 1.00 ATOM 37 O GLU A 264 -12.339 29.599 -13.923 1.00 ATOM 38 N VAL A 265 -12.709 29.777 -11.561 1.00 ATOM 37 O GLU A 264 -12.339 29.599 -13.923 1.00 ATOM 38 N VAL A 265 -12.393 29.599 -13.923 1.00 ATOM 39 CA VAL A 265 -12.393 29.599 -13.923 1.00 ATOM 39 CA VAL A 265 -12.393 29.599 -13.923 1.00 ATOM 39 CA VAL A 265 -12.393 29.599 -13.923 1.00 ATOM 39 CA VAL A 265 -12.393 29.599 -13.923 1.00 ATOM 39 CA VAL A 265 -12.393 29.599 -13.923 1.00 ATOM 39 CA VAL A 265 -12.393 29.599 -13.923 1.00 ATOM 39 CA VAL A 266 -12.590 34.829 -13.048 1.00 ATOM 39 CA			N I	HIS A	262					
ATOM 13 CB HIS A 262 -1/1.695 31.632 -14.199 1.00 ATOM 14 CG HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 15 ND1 HIS A 262 -19.391 29.908 -14.883 1.00 ATOM 16 CE1 HIS A 262 -19.744 29.220 -15.954 1.00 ATOM 17 NE2 HIS A 262 -18.082 30.538 -16.516 1.00 ATOM 18 CD2 HIS A 262 -18.082 30.538 -16.516 1.00 ATOM 20 O HIS A 262 -18.815 31.792 -12.437 1.00 ATOM 21 N LEU A 263 -16.300 32.109 -11.235 1.00 ATOM 22 CA LEU A 263 -16.300 32.109 -11.235 1.00 ATOM 23 CB LEU A 263 -16.221 33.286 -9.044 1.00 ATOM 24 CG LEU A 263 -16.866 34.666 -9.101 1.00 ATOM 25 CD1 LEU A 263 -16.866 34.666 -9.101 1.00 ATOM 26 CD2 LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 27 C LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 28 O LEU A 263 -14.497 30.672 -9.638 1.00 ATOM 30 CA GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 30 CA GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 31 CB GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 32 CG GLU A 264 -13.359 28.839 -8.952 1.00 ATOM 33 CD GLU A 264 -13.359 28.839 -8.952 1.00 ATOM 34 OE1 GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 35 OE2 GLU A 264 -14.038 28.349 -8.952 1.00 ATOM 36 C GLU A 264 -13.359 29.694 -10.251 1.00 ATOM 37 O GLU A 264 -11.161 29.596 -9.920 1.00 ATOM 38 N VAL A 265 -12.993 29.597 -11.516 1.00 ATOM 39 CA VAL A 265 -12.993 29.597 -11.516 1.00 ATOM 40 CB VAL A 265 -12.993 29.597 -11.516 1.00 ATOM 40 CB VAL A 266 -11.486 29.892 -15.064 1.00 ATOM 41 CG1 VAL A 266 -11.486 29.892 -15.064 1.00 ATOM 42 CG2 VAL A 265 -12.995 31.343 -12.257 1.00 ATOM 44 O VAL A 266 -11.486 29.892 -15.064 1.00 ATOM 50 CD2 LEU A 266 -11.486 29.892 -15.064 1.00 ATOM 51 C LEU A 266 -11.486 29.892 -15.064 1.00 ATOM 50 CD2 LEU A 266 -11.486 29.892 -15.064 1.00 ATOM 50 CD2 LEU A 266 -11.486 29.892 -15.064 1.00 ATOM 50 CD2 LEU A 266 -10.980 30.984 -12.896 1.00 ATOM 50 CD2 LEU A 266 -10.980 30.984 -12.896 1.00 ATOM 50 CD2 LEU A 266 -10.980 30.984 -12.897 1.00 ATOM 50 CD2 LEU A 266 -10.980 30.984 -12.897 1.00 ATOM 50 CD2 LEU A 266 -10.980 30.984 -12.897 1.00 ATOM 50 CD2 LEU A 266 -10.898 31.10 -10.094 1.00 ATOM 50 CD2 LEU A 266 -10.980 30.984 -12.			CA I	HIS A	262		•			
ATOM ATOM ATOM 16 CE1 HIS A 262 ATOM 16 CE1 HIS A 262 ATOM 17 NE2 HIS A 262 ATOM 18 CD2 HIS A 262 ATOM 18 CD2 HIS A 262 ATOM 19 C HIS A 262 ATOM 20 O HIS A 262 ATOM 21 N LEU A 263 ATOM 22 CA LEU A 263 ATOM 24 CG LEU A 263 ATOM 25 CD1 LEU A 263 ATOM 26 CD2 LEU A 263 ATOM 27 C LEU A 263 ATOM 28 O LEU A 263 ATOM 29 N GLU A 264 ATOM 29 N GLU A 264 ATOM 30 CA GLU A 264 ATOM 31 CB GLU A 264 ATOM 31 CB GLU A 264 ATOM 31 CB GLU A 264 ATOM 32 CG GLU A 264 ATOM 33 CB GLU A 264 ATOM 34 OEI GLU A 264 ATOM 35 OE2 GLU A 264 ATOM 36 C GLU A 264 ATOM 37 O GLU A 264 ATOM 38 N VAL A 265 ATOM 39 CA VAL A 265 ATOM 40 CB VAL A 265 ATOM 41 CG LEU A 265 ATOM 42 CG2 VAL A 265 ATOM 43 C VAL A 265 ATOM 44 CB VAL A 265 ATOM 45 CB PHE A 2667 ATOM 46 CA LEU A 2666 ATOM 47 CB LEU A 2666 ATOM 48 CG LEU A 2666 ATOM 49 CD1 LEU A 2666 ATOM 49 CD1 LEU A 2666 ATOM 40 CB VAL A 2666 ATOM 40 CB PHE A 2667 ATOM 50 CP PHE A 2667 ATOM 51 C CP PHE A 2667 ATOM 52 CP PHE A 2667 ATOM 53 CP PHE A 2667 ATOM 54 CP PHE A 2667 ATOM 55 CP PHE A 2667 ATOM 56 CP PHE A 2667 ATOM 57 CP PHE A 2667 ATOM 58 CE1 PHE A 2667 ATOM 59 CP PHE A 2667 ATOM 50 CP PHE A 2667 ATOM 50 CP PHE A 2667 ATOM 51 C CP PHE A 2667 ATOM 52 CP PHE A 2667 ATOM 53 CP PHE A 2667 ATOM 54 CP PHE A 2667 ATOM 55 CP PHE A 2667 ATOM 56 CP PHE A 2667 ATOM 57 CD1 PHE A 2667 ATOM 58 CE1 PHE A 2667 ATOM 59 CP PHE		13	CB 1	HIS A	262					59.57
ATOM 16 CE1 HIS A 262	ATOM								1.00	
ATOM ATOM ATOM ATOM ATOM ATOM ATOM ATOM	ATOM	15	ND1	HIS A	262				1.00	
ATOM 18 CD2 HIS A 262			CE1	HIS A	262					59.72
ATOM ATOM 19 C HIS A 262 ATOM 20 O HIS A 262 ATOM 21 N LEU A 263 ATOM 22 CA LEU A 263 ATOM 22 CA LEU A 263 ATOM 23 CB LEU A 263 ATOM 24 CG LEU A 263 ATOM 25 CD1 LEU A 263 ATOM 27 C LEU A 263 ATOM 28 O LEU A 263 ATOM 29 N GLU A 263 ATOM 29 N GLU A 264 ATOM 30 CA GLU A 264 ATOM 31 CB GLU A 264 ATOM 31 CB GLU A 264 ATOM 32 CG GLU A 264 ATOM 33 CB GLU A 264 ATOM 34 CE GLU A 264 ATOM 35 OE2 GLU A 264 ATOM 36 C GLU A 264 ATOM 37 O GLU A 264 ATOM 38 N VAL A 265 ATOM 39 C VAL A 265 ATOM 39 C VAL A 265 ATOM 40 CB VAL A 265 ATOM 40 CB VAL A 265 ATOM 41 CG1 VAL A 266 ATOM 42 CG LU A 266 ATOM 43 C VAL A 265 ATOM 44 O VAL A 265 ATOM 45 N LEU A 266 ATOM 46 CA LEU A 266 ATOM 47 CB LEU A 266 ATOM 48 CG LEU A 266 ATOM 49 CD1 LEU A 266 ATOM 40 CB VAL A 266 ATOM 41 CG1 VAL A 266 ATOM 42 CG LEU A 266 ATOM 43 C VAL A 265 ATOM 44 O VAL A 265 ATOM 45 N LEU A 266 ATOM 46 CA LEU A 266 ATOM 47 CB LEU A 266 ATOM 48 CG LEU A 266 ATOM 49 CD1 LEU A 266 ATOM 59 CP PHE A 267 ATOM 50 CP PHE A 267 ATOM 51 CP PHE A 267 ATOM 52 CP PHE A 267 ATOM 53 CP PHE A 267 ATOM 54 CP PHE A 267 ATOM 55 CP PHE A 267 ATOM 56 CP PHE A 267 ATOM 57 CD1 PHE A 267 ATOM 58 CP PHE A 267 ATOM 59 CP PHE A 267 ATOM 59 CP PHE A 267 ATOM 50 CP PHE A			NEZ	HIS A	262					59.13
ATOM 20				HIG V	262					59.09
ATOM 22 CA LEU A 263			-				32.162	-12.810		58.61
ATOM 23 CB LEU A 263 -15.449 32.829 -10.282 1.01 ATOM 24 CG LEU A 263 -16.221 33.286 -9.044 1.01 ATOM 25 CD1 LEU A 263 -16.866 34.666 -9.101 1.01 ATOM 26 CD2 LEU A 263 -17.642 34.934 -7.824 1.01 ATOM 27 C LEU A 263 -17.642 34.934 -7.824 1.01 ATOM 28 O LEU A 263 -15.841 35.758 -9.332 1.01 ATOM 28 O LEU A 263 -14.261 31.965 -9.840 1.01 ATOM 29 N GLU A 264 -14.497 30.672 -9.638 1.01 ATOM 30 CA GLU A 264 -14.497 30.672 -9.638 1.01 ATOM 31 CB GLU A 264 -14.497 30.672 -9.638 1.01 ATOM 31 CB GLU A 264 -14.303 28.349 -8.952 1.01 ATOM 32 CG GLU A 264 -13.450 29.748 -9.204 1.01 ATOM 33 CD GLU A 264 -13.227 27.462 -8.006 1.01 ATOM 34 OE1 GLU A 264 -13.691 25.995 -8.002 1.01 ATOM 35 OE2 GLU A 264 -14.800 25.693 -7.476 1.01 ATOM 36 C GLU A 264 -14.800 25.693 -7.476 1.01 ATOM 37 O GLU A 264 -11.161 29.596 -9.920 1.01 ATOM 38 N VAL A 265 -12.934 25.135 -8.534 1.01 ATOM 39 CA VAL A 265 -12.709 29.797 -11.516 1.01 ATOM 30 CB VAL A 265 -12.709 29.797 -11.516 1.01 ATOM 40 CB VAL A 265 -12.393 29.559 -13.923 1.01 ATOM 41 CG1 VAL A 265 -12.393 29.559 -13.923 1.01 ATOM 42 CG2 VAL A 265 -11.722 29.766 -12.574 1.01 ATOM 43 C VAL A 265 -11.780 34.586 -12.194 1.025 1.01 ATOM 44 O VAL A 265 -11.436 29.892 -15.064 1.01 ATOM 45 N LEU A 266 -11.780 33.433 -12.254 1.01 ATOM 46 CA LEU A 266 -11.780 34.586 -12.145 1.01 ATOM 47 CB LEU A 266 -11.780 34.586 -12.146 1.01 ATOM 49 CD1 LEU A 266 -11.780 34.586 -12.146 1.01 ATOM 50 CD2 LEU A 266 -11.780 34.423 -11.104 1.01 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.01 ATOM 50 CD2 LEU A 266 -9.981 32.773 -10.094 1.01 ATOM 50 CD2 LEU A 266 -9.981 32.773 -10.094 1.01 ATOM 50 CD2 LEU A 266 -9.981 32.773 -10.094 1.01 ATOM 50 CD2 LEU A 266 -9.981 32.773 -10.094 1.01 ATOM 50 CD2 LEU A 266 -9.981 32.773 -10.094 1.01 ATOM 50 CD2 LEU A 266 -9.770 33.556 -11.108 1.01 ATOM 50 CD2 LEU A 266 -9.770 33.556 -11.108 1.01 ATOM 50 CD2 LEU A 266 -9.770 33.556 -11.108 1.01 ATOM 50 CD2 LEU A 266 -9.770 33.556 -11.108 1.01 ATOM 50 CD2 LEU A 266 -9.770 33.556 -11.108 1.01 ATOM 50 CD2 LEU A 266 -9.770 33.556 -11.108 1.01 A							32.109	-11.235		58.77
ATOM 24 CG LEU A 263						-15.449	32.829			58.96
ATOM 24 CG LEU A 263 -16.866 34.666 -9.101 1.07 ATOM 25 CD1 LEU A 263 -17.642 34.934 -7.824 1.00 ATOM 26 CD2 LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 27 C LEU A 263 -15.841 35.758 -9.332 1.00 ATOM 28 O LEU A 263 -13.154 32.463 -9.682 1.00 ATOM 29 N GLU A 264 -14.497 30.672 -9.638 1.00 ATOM 30 CA GLU A 264 -14.497 30.672 -9.638 1.00 ATOM 31 CB GLU A 264 -14.497 30.672 -9.638 1.00 ATOM 32 CG GLU A 264 -14.497 30.672 -9.638 1.00 ATOM 32 CG GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 33 CD GLU A 264 -13.227 27.462 -8.006 1.00 ATOM 34 OEI GLU A 264 -13.691 25.995 -8.006 1.00 ATOM 35 OE2 GLU A 264 -14.800 25.693 -7.476 1.00 ATOM 36 C GLU A 264 -12.339 29.694 -10.251 1.00 ATOM 37 O GLU A 264 -11.161 29.596 -9.920 1.00 ATOM 38 N VAL A 265 -12.709 29.797 -11.516 1.00 ATOM 38 N VAL A 265 -12.709 29.797 -11.516 1.00 ATOM 39 CA VAL A 265 -12.393 29.559 -13.923 1.00 ATOM 40 CB VAL A 265 -12.393 29.559 -13.923 1.00 ATOM 41 CG1 VAL A 265 -11.436 29.892 -15.064 1.00 ATOM 42 CG2 VAL A 265 -12.905 28.140 -14.025 1.00 ATOM 44 O VAL A 265 -12.905 28.140 -14.025 1.00 ATOM 45 N LEU A 266 -11.488 32.164 -12.896 1.00 ATOM 46 CA LEU A 266 -10.780 33.433 -12.254 1.00 ATOM 47 CB LEU A 266 -11.780 34.586 -12.145 1.00 ATOM 48 CG LEU A 266 -11.780 34.423 -11.140 1.00 ATOM 50 CD2 LEU A 266 -11.780 34.423 -11.140 1.00 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.00 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.00 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.00 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.00 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.00 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.00 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.00 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.00 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.00 ATOM 50 CD2 LEU A 266 -10.780 34.423 -11.140 1.00 ATOM 50 CD2 LEU A 266 -10.780 34.423 -11.140 1.00 ATOM 50 CD2 LEU A 266 -10.780 34.423 -11.140 1.00 ATOM 50 CD2 LEU A 266 -10.780 36.617 -7.550 1.00 ATOM 50 CD2 LEU A 266 -10.498 34.119 -7.397 1.00 ATOM 50 CD2 PHE A 267 -9.914 32.713 -10.0			CB	LEU A	. 263			-		
ATOM 25 CD1 LEU A 263										58.28 57.90
ATOM 26 CD2 LEU A 263 -14.261 31.965 -9.840 1.00 ATOM 28 O LEU A 263 -13.154 32.463 -9.682 1.00 ATOM 29 N GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 30 CA GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 31 CB GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 32 CG GLU A 264 -13.450 29.748 -9.204 1.00 ATOM 33 CD GLU A 264 -13.691 25.995 -8.006 1.00 ATOM 34 OE1 GLU A 264 -13.691 25.995 -8.002 1.00 ATOM 35 OE2 GLU A 264 -12.934 25.135 -8.594 1.00 ATOM 36 C GLU A 264 -12.934 25.135 -8.594 1.00 ATOM 37 O GLU A 264 -11.161 29.596 -9.920 1.00 ATOM 38 N VAL A 265 -12.709 29.797 -11.516 1.00 ATOM 39 CA VAL A 265 -11.722 29.766 -12.574 1.00 ATOM 40 CB VAL A 265 -11.722 29.766 -12.574 1.00 ATOM 40 CB VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 41 CG1 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 42 CG2 VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 44 O VAL A 265 -10.878 31.034 -12.259 1.0 ATOM 45 N LEU A 266 -10.780 33.433 -12.254 1.0 ATOM 46 CA LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 47 CB LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 49 CD1 LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 50 CD2 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -12.349 34.299 -33.408 1.0 ATOM 50 CD2 LEU A 266 -12.349 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -12.367 -9.881 32.790 -7.656 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.009 1.0 ATOM 50 CD2 PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 50 CD2 PHE A		25	CD1	LEU A	263				-	57.75
ATOM 28 O LEU A 263 -13.154 32.463 -9.682 1.0 ATOM 29 N GLU A 264 -14.497 30.672 -9.638 1.0 ATOM 30 CA GLU A 264 -13.450 29.748 -9.204 1.0 ATOM 31 CB GLU A 264 -14.038 28.349 -8.952 1.0 ATOM 31 CB GLU A 264 -14.038 28.349 -8.952 1.0 ATOM 32 CG GLU A 264 -13.227 27.462 -8.006 1.0 ATOM 33 CD GLU A 264 -13.691 25.995 -8.002 1.0 ATOM 36 C GLU A 264 -14.800 25.693 -7.476 1.0 ATOM 36 C GLU A 264 -12.339 29.694 -10.251 1.0 ATOM 37 O GLU A 264 -11.161 29.596 -9.920 1.0 ATOM 38 N VAL A 265 -12.709 29.797 -11.516 1.0 ATOM 39 CA VAL A 265 -12.709 29.797 -11.516 1.0 ATOM 40 CB VAL A 265 -11.722 29.766 -12.574 1.0 ATOM 41 CG1 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 42 CG2 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 44 O VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 44 O VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 45 N LEU A 266 -10.878 31.034 -12.259 1.0 ATOM 46 CA LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 47 CB LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 49 CD1 LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 49 CD1 LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 49 CD1 LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 50 CD2 LEU A 266 -13.498 36.026 -13.2254 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 LEU A 266 -9.9777 33.556 -11.108 1.0 ATOM 50 CD2 CD2 CD3 ATOM	MOTA		CD2	LEU A	. 263					59.44
ATOM 29 N GLU A 264 -14.497 30.672 -9.638 1.00 ATOM 30 CA GLU A 264 -13.450 29.748 -9.204 1.0 ATOM 31 CB GLU A 264 -14.038 28.349 -8.952 1.0 ATOM 32 CG GLU A 264 -13.227 27.462 -8.006 1.0 ATOM 33 CD GLU A 264 -13.691 25.995 -8.002 1.0 ATOM 34 OE1 GLU A 264 -14.800 25.693 -7.476 1.0 ATOM 35 OE2 GLU A 264 -12.339 29.694 -10.251 1.0 ATOM 36 C GLU A 264 -11.161 29.596 -9.920 1.0 ATOM 37 O GLU A 264 -11.161 29.596 -9.920 1.0 ATOM 38 N VAL A 265 -12.709 29.776 -12.574 1.0 ATOM 39 CA VAL A 265 -11.722 29.766 -12.574 1.0 ATOM 40 CB VAL A 265 -11.722 29.766 -12.574 1.0 ATOM 41 CG1 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 42 CG2 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 43 C VAL A 265 -12.905 28.140 -14.025 1.0 ATOM 44 O VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 45 N LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 46 CA LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 47 CB LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 48 CG LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 49 CD1 LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 53 N PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 55 CB PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 56 CG PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 57 CD1 PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 58 CE1 PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 59 CZ PHE A 267 -9.035 32.758 -7.500 1.0 ATOM 59 CZ PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 50 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 50 CP2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 50 CP2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 50 CP2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 60 CE2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 60 CE2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 60 CP2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 60 CP2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 60 CP3 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267	MOTA			LEU A	263			_		59.40
ATOM 30 CA GLU A 264 -13.450 29.748 -9.204 1.0 ATOM 31 CB GLU A 264 -14.038 28.349 -8.952 1.0 ATOM 32 CG GLU A 264 -13.227 27.462 -8.006 1.0 ATOM 33 CD GLU A 264 -13.691 25.995 -8.002 1.0 ATOM 34 OE1 GLU A 264 -13.691 25.995 -8.002 1.0 ATOM 35 OE2 GLU A 264 -12.339 29.694 -10.251 1.0 ATOM 36 C GLU A 264 -12.339 29.694 -10.251 1.0 ATOM 37 O GLU A 264 -11.161 29.596 -9.920 1.0 ATOM 38 N VAL A 265 -12.709 29.797 -11.516 1.0 ATOM 39 CA VAL A 265 -11.722 29.766 -11.574 1.0 ATOM 40 CB VAL A 265 -11.722 29.766 -12.574 1.0 ATOM 41 CG1 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 42 CG2 VAL A 265 -12.995 28.140 -14.025 1.0 ATOM 43 C VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 44 O VAL A 265 -10.878 31.034 -12.259 1.0 ATOM 45 N LEU A 266 -10.878 31.034 -12.259 1.0 ATOM 46 CA LEU A 266 -10.780 33.433 -12.254 1.0 ATOM 47 CB LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 48 CG LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 49 CD1 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 52 O LEU A 266 -8.907 34.423 -11.104 1.0 ATOM 53 N PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 54 CA PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 55 CB PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 56 CG PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 57 CD1 PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 58 CE1 PHE A 267 -1.1.812 34.368 -7.719 1.0 ATOM 58 CE1 PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 59 CZ PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 60 CE2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0			0	LEU A	263					60.29
ATOM 31 CB GLU A 264 -14.038 28.349 -8.952 1.0 ATOM 32 CG GLU A 264 -13.227 27.462 -8.006 1.0 ATOM 33 CD GLU A 264 -13.691 25.995 -8.002 1.0 ATOM 34 OE1 GLU A 264 -14.800 25.693 -7.476 1.0 ATOM 35 OE2 GLU A 264 -12.934 25.135 -8.534 1.0 ATOM 36 C GLU A 264 -12.934 25.135 -8.534 1.0 ATOM 37 O GLU A 264 -12.339 29.694 -10.251 1.0 ATOM 38 N VAL A 265 -12.709 29.797 -11.516 1.0 ATOM 38 N VAL A 265 -11.722 29.766 -12.574 1.0 ATOM 39 CA VAL A 265 -11.722 29.766 -12.574 1.0 ATOM 40 CB VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 41 CG1 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 42 CG2 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 43 C VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 44 O VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 45 N LEU A 266 -10.780 33.433 -12.254 1.0 ATOM 46 CA LEU A 266 -10.780 33.433 -12.254 1.0 ATOM 47 CB LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 49 CD1 LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 49 CD1 LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -12.590 34.829 -13.408 1.0 ATOM 50 CD2 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 51 C LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 52 O LEU A 266 -9.977 33.556 -11.108 1.0 ATOM 54 CA PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 55 CB PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 56 CG PHE A 267 -9.935 32.758 -8.931 1.0 ATOM 57 CD1 PHE A 267 -9.935 32.758 -8.931 1.0 ATOM 58 CE1 PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 59 CZ PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 59 CZ PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 50 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 50 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 60 CE2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.974 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -9.974 31.595 -8.858 1.0				GLU A	264					60.91
ATOM ATOM ATOM ATOM ATOM ATOM ATOM ATOM			_	CLII A	264				1.00	61.72
ATOM ATOM ATOM ATOM ATOM ATOM ATOM ATOM				CIJI A	264					64.54
ATOM 34 OE1 GLU A 264 -14.800 25.693 -7.476 1.0 ATOM 35 OE2 GLU A 264 -12.934 25.135 -8.534 1.0 ATOM 36 C GLU A 264 -12.339 29.694 -10.251 1.0 ATOM 37 O GLU A 264 -11.161 29.596 -9.920 1.0 ATOM 38 N VAL A 265 -12.709 29.797 -11.516 1.0 ATOM 40 CB VAL A 265 -11.702 29.766 -12.574 1.0 ATOM 41 CG1 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 42 CG2 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 43 C VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 44 CG1 VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 45 N LEU A 265 -10.878 31.034 -12.599 1.0 ATOM 46 CA LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 46 CA LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 47 CB LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 49 CD1 LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 51 C LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 52 O LEU A 266 -9.9914 32.713 -10.094 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 56 CG PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 57 CD1 PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 58 CE1 PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 59 CZ PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 59 CZ PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 59 CZ PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 59 CZ PHE A 267 -9.745 35.615 -7.500 1.0 ATOM 60 CE2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1				GLU A	264		25.995		1.00	68.63
ATOM 35 OE2 GLU A 264 -12.934 25.135 -8.534 1.0 ATOM 36 C GLU A 264 -12.339 29.694 -10.251 1.0 ATOM 37 O GLU A 264 -11.161 29.596 -9.920 1.0 ATOM 38 N VAL A 265 -12.709 29.797 -11.516 1.0 ATOM 39 CA VAL A 265 -12.709 29.797 -11.516 1.0 ATOM 40 CB VAL A 265 -12.393 29.559 -13.923 1.0 ATOM 41 CG1 VAL A 265 -12.393 29.559 -13.923 1.0 ATOM 42 CG2 VAL A 265 -12.393 29.559 -13.923 1.0 ATOM 42 CG2 VAL A 265 -12.393 29.559 -13.923 1.0 ATOM 43 C VAL A 265 -12.395 28.140 -14.025 1.0 ATOM 44 O VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 45 N LEU A 265 -9.689 30.984 -12.896 1.0 ATOM 46 CA LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 47 CB LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 48 CG LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 49 CD1 LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 49 CD1 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 50 CD2 LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 51 C LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 52 O LEU A 266 -9.914 32.713 -10.094 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 57 CD1 PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 58 CE1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 59 CZ PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 50 CD2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 50 CD2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.758 70 587 1.0				GLU A	264					69.87
ATOM 36 C GLU A 264 -12.339 29.594 -10.251 1.0 ATOM 37 O GLU A 264 -11.161 29.596 -9.920 1.0 ATOM 38 N VAL A 265 -12.709 29.797 -11.516 1.0 ATOM 39 CA VAL A 265 -11.722 29.766 -12.574 1.0 ATOM 40 CB VAL A 265 -12.393 29.559 -13.923 1.0 ATOM 41 CG1 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 42 CG2 VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 43 C VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 44 O VAL A 265 -9.689 30.984 -12.896 1.0 ATOM 45 N LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 46 CA LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 47 CB LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 48 CG LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 49 CD1 LEU A 266 -12.590 34.829 -13.408 1.0 ATOM 49 CD1 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 52 O LEU A 266 -8.907 34.423 -11.140 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 55 CB PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 56 CG PHE A 267 -9.981 32.790 -7.656 1.0 ATOM 57 CD1 PHE A 267 -9.981 32.790 -7.656 1.0 ATOM 58 CE1 PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 59 CZ PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 50 CD2 PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 56 CG PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 57 CD1 PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 58 CE1 PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 59 CZ PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 50 CD2 PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 50 CD2 PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 57 CD1 PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 58 CE1 PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 59 CZ PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 59 CZ PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 60 CD2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.9745 35.138 -9.987 1.0				GLU A	264					70.91 60.26
ATOM ATOM ATOM ATOM ATOM ATOM ATOM ATOM		36	С	GLU A	264					60.28
ATOM 39 CA VAL A 265 -11.722 29.766 -12.574 1.0 ATOM 40 CB VAL A 265 -12.393 29.559 -13.923 1.0 ATOM 41 CG1 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 42 CG2 VAL A 265 -12.905 28.140 -14.025 1.0 ATOM 43 C VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 44 O VAL A 265 -9.689 30.984 -12.896 1.0 ATOM 45 N LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 46 CA LEU A 266 -11.780 33.433 -12.254 1.0 ATOM 47 CB LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 48 CG LEU A 266 -11.780 34.829 -13.408 1.0 ATOM 49 CD1 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 51 C LEU A 266 -13.655 35.012 -14.604 1.0 ATOM 52 O LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 57 CD1 PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 58 CE1 PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 58 CE1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 58 CE1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 AT	MOTA	37		GLU A	264		29.596			59.34
ATOM 40 CB VAL A 265 -12.393 29.559 -13.923 1.0 ATOM 41 CG1 VAL A 265 -11.436 29.892 -15.064 1.0 ATOM 42 CG2 VAL A 265 -12.905 28.140 -14.025 1.0 ATOM 43 C VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 44 O VAL A 265 -9.689 30.984 -12.896 1.0 ATOM 45 N LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 46 CA LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 47 CB LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 48 CG LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 49 CD1 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -1.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 52 O LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 57 CD1 PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 58 CE1 PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 58 CE1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -9.758 1.0						-12.709	29.757	-12.574		58.79
ATOM 41 CG1 VAL A 265										58.56
ATOM 42 CG2 VAL A 265 -12.905 28.140 -14.025 1.0 ATOM 43 C VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 44 O VAL A 265 -9.689 30.984 -12.896 1.0 ATOM 45 N LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 46 CA LEU A 266 -10.780 33.433 -12.254 1.0 ATOM 47 CB LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 48 CG LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 49 CD1 LEU A 266 -12.590 34.829 -13.408 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 52 O LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 57 CD1 PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 58 CE1 PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 59 CZ PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 59 CZ PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 60 CE2 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 60 CE2 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -9.587 1.0							29.892	-15.064		58.68
ATOM 43 C VAL A 265 -10.878 31.034 -12.599 1.0 ATOM 44 O VAL A 265 -9.689 30.984 -12.896 1.0 ATOM 45 N LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 46 CA LEU A 266 -10.780 33.433 -12.254 1.0 ATOM 47 CB LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 48 CG LEU A 266 -12.590 34.829 -13.408 1.0 ATOM 49 CD1 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 52 O LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 57 CD1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 58 CE1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 59 CZ PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 60 CE2 PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -9.745 35.138 -9.587 1.0									1.00	57.58
ATOM 44 O VAL A 265				VAL	265		31.034	-12.599		58.95
ATOM 45 N LEU A 266 -11.488 32.164 -12.282 1.0 ATOM 46 CA LEU A 266 -10.780 33.433 -12.254 1.0 ATOM 47 CB LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 48 CG LEU A 266 -12.590 34.829 -13.408 1.0 ATOM 49 CD1 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 52 O LEU A 266 -8.907 34.423 -11.140 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 57 CD1 PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 58 CE1 PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 59 CZ PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 59 CZ PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 60 CE2 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 61 CD2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0							30.984	-12.896		58.69
ATOM 46 CA LEU A 266 -10.780 33.433 -12.254 1.0 ATOM 47 CB LEU A 266 -11.780 34.586 -12.145 1.0 ATOM 48 CG LEU A 266 -12.590 34.829 -13.408 1.0 ATOM 49 CD1 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 52 O LEU A 266 -8.907 34.423 -11.140 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 57 CD1 PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 58 CE1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 59 CZ PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0				LEU A	A 266		32.164	-12.282	1.00	59.10
ATOM 48 CG LEU A 266 -12.590 34.829 -13.408 1.0 ATOM 49 CD1 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 52 O LEU A 266 -8.907 34.423 -11.140 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 57 CD1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 58 CE1 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0				LEU A	A 266		33.433	-12.254	1.00	
ATOM 48 CG LEU A 266 -12.590 34.829 -13.408 1.0 ATOM 49 CD1 LEU A 266 -13.498 36.026 -13.226 1.0 ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 52 O LEU A 266 -8.907 34.423 -11.140 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 57 CD1 PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 58 CE1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 59 CZ PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0		47	CB	LEU A	A 266		34.586	-12.145		59.85 59.43
ATOM 50 CD2 LEU A 266 -11.655 35.012 -14.604 1.0 ATOM 51 C LEU A 266 -9.777 33.556 -11.108 1.0 ATOM 52 O LEU A 266 -8.907 34.423 -11.140 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 57 CD1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 58 CE1 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0			CG	LEU A	A 266		34.829	-13.400	1 00	58.82
ATOM 51 C LEU A 266			CD1	LEU !	A 266		35.020	-14 604		58.96
ATOM 52 O LEU A 266 -8.907 34.423 -11.140 1.0 ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 57 CD1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 58 CE1 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0				LEO A	A 266					60.75
ATOM 53 N PHE A 267 -9.914 32.713 -10.094 1.0 ATOM 54 CA PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 57 CD1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 58 CE1 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0				PEO V	A 266					60.71
ATOM 54 CA PHE A 267 -9.035 32.758 -8.931 1.0 ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 57 CD1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 58 CE1 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0										62.00
ATOM 55 CB PHE A 267 -9.881 32.790 -7.656 1.0 ATOM 56 CG PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 57 CD1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 58 CE1 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0				PHE	A 267					63.40
ATOM 56 CG PHE A 267 -10.498 34.119 -7.397 1.0 ATOM 57 CD1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 58 CE1 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0				PHE	A 267		32.790	-7.656		63.54
ATOM 57 CD1 PHE A 267 -11.812 34.368 -7.719 1.0 ATOM 58 CE1 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0			CG	PHE	A 267	-10.498	34.119	-7.397		64.83
ATOM 58 CE1 PHE A 267 -12.367 35.615 -7.500 1.0 ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0			CD1	PHE .	A 267					66.41
ATOM 59 CZ PHE A 267 -11.605 36.617 -6.969 1.0 ATOM 60 CE2 PHE A 267 -10.298 36.382 -6.649 1.0 ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0			CE1	PHE .	A 267					67.05
ATOM 61 CD2 PHE A 267 -9.745 35.138 -6.864 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0		59			A 267		36.617			67.09 67.35
ATOM 61 CD2 PRE A 267 -8.042 31.595 -8.858 1.0 ATOM 62 C PHE A 267 -8.042 31.595 -8.858 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0	ATOM			PHE.	A 267					66.42
ATOM 62 C PRE A 267 -7.031 31.680 -8.158 1.0 ATOM 63 O PHE A 267 -7.031 31.680 -8.158 1.0				PHE	A 267		33.136			64.32
ATOM 63 0 FRE A 200 9 325 30 519 -9 587 1.0				PHE.	A 201 A 267				1.00	65.16
ATOM 04 N GEN II 200				CI-M	A 268				1.00	64.99
	ATOM	04	14	٧٠٠٠٧						

 \mathbf{z}

- mon	65 CA GLN A 268	-7.514 2	29.299 -9.542	
ATOM	65 CA GLN A 268 66 CB GLN A 268	-7.800 2	28.433 -10.770	1.00 65.80
ATOM ATOM	67 CG GLN A 268	-7.456 2	26.956 -10.580	1.00 67.88
ATOM	68 CD GLN A 268		26.122 -11.809	1.00 70.56
ATOM	69 OE1 GLN A 268		26.568 -12.683	1.00 72.72
ATOM	70 NE2 GLN A 268		24.919 -11.89	1 1.00 71.16 5 1.00 64.81
ATOM	71 C GLN A 268		29.518 -9.41	
MOTA	72 O GLN A 268	-5.350	28.832 -8.63	
MOTA	73 N GLY A 269		30.451 -10.189 30.686 -10.12	
MOTA	74 CA GLY A 269		31.020 -8.72	
MOTA	75 C GLY A 269		30.147 -7.97	
ATOM	76 O GLY A 269 77 N PRO A 270		32.295 -8.36	
ATOM			32.784 -7.04	6 1.00 60.71
MOTA	78 CA PRO A 270 79 CB PRO A 270		34.203 -7.01	
ATOM ATOM	80 CG PRO A 270		34.625 -8.46	0 1.00 61.54
ATOM	81 CD PRO A 270		33.374 -9.23	8 1.00 61.80
ATOM	82 C PRO A 270		31.980 -5.89	
ATOM	83 O PRO A 270		31.832 - 4.87	
ATOM	84 N ALA A 271		31.464 -6.03	
ATOM	85 CA ALA A 271		30.679 -4.95 30.115 -5.33	T
ATOM	86 CB ALA A 271		30.115 -5.33 29.553 -4.62	
ATOM	87 C ALA A 271	-4.642 -4.414	29.277 -3.46	
MOTA	88 O ALA A 271		28.906 -5.66	
ATOM	89 N GLUA 272 90 CA GLUA 272	-3.219	27.766 -5.54	
ATOM		-2.898	27.199 -6.92	6 1.00 55.29
MOTA	91 CB GLU A 272 92 CG GLU A 272	-2.191	25.854 -6.93	
ATOM ATOM	93 CD GLU A 272	-3.117	24.691 -6.58	
ATOM	94 OE1 GLU A 272	-4.000	24.868 -5.69	
ATOM	95 OE2 GLU A 272	-2.966	23.598 - 7.20	
ATOM	96 C GLU A 272	-1.923	28.139 -4.81	
ATOM	97 O GLU A 272	-1.420	27.370 -4.01	
MOTA	98 N LEUA 273	-1.392	29.323 -5.10 29.775 -4.44	T
ATÖM	99 CA LEU A 273	-0.187	31.091 -5.02	
MOTA	100 CB LEU A 273	0.295 0.578	31.167 -6.52	
ATOM	101 CG LEU A 273 102 CD1 LEU A 273	1.291	32.486 -6.81	
ATOM		1.400	29.983 -7.00	7 1.00 56.45
ATOM ATOM	103 CD2 LEU A 273 104 C LEU A 273	-0.489	30.012 -2.98	
ATOM	105 O LEU A 273	0.302	29.668 -2.10	
ATOM	106 N GLUA 274	-1.638	30.629 - 2.72	
ATOM	107 CA GLU A 274	-2.025	30.937 -1.36	
ATOM	108 CB GLU A 274	-3.276	31.827 -1.32	
ATOM	109 CG GLU A 274	-3.526	32.505 0.03 33.359 0.48	
MOTA	110 CD GLU A 274	-2.357 -1.827	34.142 -0.34	
ATOM	111 OE1 GLU A 274	-1.974	33 236 1.60	55 1.00 56.29
ATOM	112 OE2 GLU A 274 113 C GLU A 274	-2.248	29.627 -0.62	29 1.00 48.42
MOTA	113 C GLU A 274 114 O GLU A 274	-1.817	29.475 0.50	05 1.00 48.21
ATOM	115 N HIS A 275	-2.879	28.668 -1.28	35 1.00 47.05
ATOM ATOM	116 CA HIS A 275	-3.148	27.394 - 0.63	
ATOM	117 CB HIS A 275	-3.928	26.445 - 1.5	
ATOM	118 CG HIS A 275	-4.241	25.113 - 0.9	
ATOM	119 ND1 HIS A 275	-5.321	24.914 -0.0	
ATOM	120 CE1 HIS A 275	-5.360	23.647 0.3 23.009 -0.2	
MOTA	121 NE2 HIS A 275	-4.345	23.009 -0.2 23.903 -1.0	
ATOM	122 CD2 HIS A 275	-3.631 -1.857	26.721 -0.1	
ATOM	123 C HIS A 275 124 O HIS A 275	-1.766	26.218 0.9	
MOTA		-0.866	26.692 -1.0	78 1.00 44.20
ATOM	125 N LEU A 276 126 CA LEU A 276	0.405	26.056 -0.7	62 1.00 43.43
ATOM ATOM	127 CB LEU A 276	1.243	25.889 -2.0	
ATOM	128 CG LEU A 276	2.652	25.291 -1.8	
ATOM	129 CD1 LEU A 276	2.568	23.818 -1.5	
ATOM	130 CD2 LEU A 276	3.486	25.536 -3.1	27 1.00 43.26

						1 170	26.881	0.310	1.00 42.47
ATOM	131	C	LEU A			1.172 1.879	26.346	1.153	1.00 40.97
MOTA	132	0	LEU A			1.035	28.190	0.302	1.00 41.76
ATOM	133	N	ALA A	2//		1.737	28.961	1.324	1.00 41.55
ATOM	134	CA	ALA A	211		1.716	30.419	1.004	1.00 41.80
ATOM	135	CB	ALA A	211		1.124	28.718	2.699	1.00 41.51
ATOM	136	C	ALA A	2//		1.832	28.631	3.708	1.00 41.21
MOTA	137	0	ALA A	2//			28.545	2.734	1.00 41.43
MOTA	138	N	GLN A			0.192	28.331	4.000	1.00 41.87
ATOM	139	CA	GLN A			0.870	28.610	3.879	1.00 42.96
MOTA	140	CB	GLN A	278		-2.373	30.122	3.749	1.00 45.63
MOTA	141	CG	GLN A			-2.684	30.122	3.501	1.00 49.42
ATOM	142	CD	GLN A			-4.182	29.751	3.921	1.00 52.18
MOTA	143	OE1	GLN A	278		-5.098	31.605	2.836	1.00 50.77
MOTA	144		GLN A	2/8		-4.410	26.945	4.521	1.00 40.99
MOTA	145	C	GLN A	2/8		-0.570 -0.411	26.736	5.719	1.00 40.26
MOTA	146	0	GLN A	278		-0.411	25.993	3.621	1.00 40.42
ATOM	147	N	ASN A			-0.449	24.635	4.021	1.00 40.51
MOTA	148	CA	ASN A			-0.075	23.755	2.795	1.00 41.05
MOTA	149	CB	ASN A	270	_	0.276	22.322	3.120	1.00 44.76
ATOM	150	CG	ASN A	270	_	-0.554	21.573	3.640	1.00 48.82
MOTA	151	ODI	ASN A	273	_	1.522	21.922	2.818	1.00 51.37
MOTA	152		ASN A	279		1.242	24.550	4.702	1.00 39.60
MOTA	153	C	ASN A	279		1.411	23.920	5.746	1.00 40.22
MOTA	154	0	ASN A	200		2.219	25.170	4.073	1.00 38.39
MOTA	155	N	ILE A	200		3.563	25.150	4.550	1.00 37.67
MOTA	156	CA	ILE A	200		4.493	25.612	3.419	1.00 37.61
MOTA	157	CB				4.506	24.532	2.322	1.00 38.20
ATOM	158	CGT	ILE A	200		5.666	24.586	1.341	1.00 39.82
ATOM	159	CDI	ILE A	200		5.892	25.864	3.974	1.00 38.20
ATOM	160		ILE A	280		3.697	25.986	5.823	1.00 36.72
ATOM	161	C	ILE A			4.355	25.583	6.765	1.00 35.34
ATOM	162	0	SER A			3.060	27.146	5.842	1.00 36.72
ATOM	163	N CA	SER A	281		3.018	27.979	7.043	1.00 36.93
ATOM	164 165	CE	SER ?	201		2.091	29.161	6.831	1.00 37.23
ATOM	166	og	SER A	281		2.681	30.069	5.909	1.00 38.94
MOTA	167	C	SER A			2.543	27.219	8.237	1.00 36.20
ATOM	168	ŏ	SER A	281		3.131	27.298	9.295	1.00 35.96
MOTA	169	N	LYS A			1.467	26.470	8.068	1.00 36.67
ATOM ATOM	170	CA	LYS 2			0.880	25.704	9.158	1.00 37.15
ATOM	171	CB	LYS A	282		-0.479	25.107	8.730	1.00 38.10
ATOM	172	CG	LYS A	A 282		-1.305	24.498	9.860	1.00 40.15
ATOM	173	CD	LYS	A 282		-2.704	24.142	9.337	1.00 46.19
ATOM	174	CE	LYS	A 282		-3.414	23.021	10.139	1.00 49.27
ATOM	175	NZ	LYS	A 282		-3.455	21.732	9.376	1.00 51.98
ATOM	176	C		A 282		1.794	24.585	9.604	1.00 36.50
ATOM	177	ō	LYS 2	A 282		1.940	24.307	10.798	1.00 35.79
ATOM	178	N	SER A	A 283		2.409	23.916	8.643	1.00 35.63
ATOM	179	CA	SER I	A 283		3.316	22.836	8.997	1.00 34.48
ATOM	180	CB	SER I	A 283		3.848	22.181	7.744	1.00 34.45
ATOM	181	OG	SER 2	A 283		2.754	21.707	7.003	1.00 34.06
MOTA	182	C	SER	A 283		4.441	23.381	9.830	1.00 33.76
ATOM	183	0	SER :	A 283		4.830	22.758	10.789	1.00 33.46
ATOM	184	N	HIS .	A 284		4.943	24.552	9.471	1.00 33.35
ATOM	185	CA	HIS .	A 284		6.007	25.195	10.224	1.00 34.42
ATOM	186	CB		A 284		6.402	26.460	9.513	1.00 34.00
ATOM	187	CG		A 284		7.306	27.355	10.288	1.00 34.20
ATOM	188	ND:	HIS.	A 284		8.677	27.240	10.249	1.00 32.90
ATOM	189	CE	L HIS	A 284		9.221	28.201	10.968	1.00 33.90
ATOM	190	NE:	HIS.	A 284		8.249	28.946	11.472	1.00 35.01
MOTA	191		HIS	A 284		7.042	28.448	11.045	1.00 36.29 1.00 35.30
MOTA	192	C	HIS	A 284		5.629	25.530	11.660	1.00 35.30 1.00 34.75
MOTA	193	0	HIS	A 284		6.391	25.244	12.589 11.824	1.00 34.75
MOTA	194	N	LEU	A 285		4.469	26.172	13.136	1.00 36.71
MOTA	195	CA		A 285		3.947	26.548	12.997	1.00 37.40
ATOM	196	СВ	FEA	A 285		2.579	27.208	12.771	

0 or sold one of the condition of the

						05 635	14 272	1.00 41.84
MOTA	197	CG	LEU A	. 285	1.838	27.637	14.272 14.913	1.00 42.97
MOTA	198	CD1	LEU A	285	2.525	28.826		1.00 43.37
MOTA	199		LEU A		0.385	27.982	13.934	1.00 43.37
MOTA	200	C	LEU A		3.846	25.351	14.046 15.206	1.00 37.27
MOTA	201	0	LEU A		4.279	25.403		1.00 36.60
ATOM	202	N	GLU A		3.369	24.237	13.510	1.00 36.00
MOTA	203	CA	GLU A		3.134	23.058	14.337	1.00 37.46
ATOM	204	CB	GLU A	286	1.988	22.229	13.722	1.00 37.40
ATOM	205	CG	GLU A		0.751	23.091	13.462	1.00 42.20
ATOM	206	CD	GLU A		-0.487	22.289	13.142	1.00 48.23
MOTA	207	OE1	GLU A		-0.343	21.219	12.510 13.534	1.00 52.12
MOTA	208	OE2	GLU A		-1.601	22.726		1.00 35.80
MOTA	209	С	GLU A		4.350	22.157	14.572 15.303	1.00 34.55
MOTA	210	0	GLU A	286	4.231	21.190 22.439	13.931	1.00 34.46
MOTA	211	N	THR A		5.485		14.118	1.00 34.18
MOTA	212	CA	THR A	287	6.684	21.616	12.814	1.00 33.50
MOTA	213	CB	THR F	287	7.154	20.957	11.807	1.00 30.59
MOTA	214		THR A	287	7.367	21.952	12.250	1.00 34.40
MOTA	215	CG2	THR A		6.122	20.050	14.670	1.00 34.80
MOTA	216	C	THR A	287	7.879	22.382 21.849	14.681	1.00 35.10
MOTA	217	0	THR A	287	8.965	23.638	15.047	1.00 35.78
MOTA	218	N	CYS A		7.709	24.346	15.740	1.00 36.72
MOTA	219	CA	CYS A		8.764	25.851	15.552	1.00 36.32
ATOM	220	CB	CYS A	288	8.642 9.235	26.481	13.966	1.00 39.84
MOTA	221	SG	CYS A	288	8.682	23.996	17.230	1.00 36.71
MOTA	222	C	CYS I	1 288	7.602	23.895	17.792	1.00 36.87
MOTA	223	0	CYS Z		9.830	23.812	17.866	1.00 37.19
MOTA	224	N	GLN A		9.862	23.516	19.278	1.00 37.25
ATOM	225	CA		A 289	11.279	23.153	19.694	1.00 37.24
MOTA	226	CB		A 289	11.409	22.864	21.168	1.00 38.95
ATOM	227	CG		A 289	12.661	22.072	21.551	1.00 40.39
MOTA	228	CD		A 289 A 289	13.694	22.091	20.847	1.00 39.04
ATOM	229	OE1	GLIV A	A 289	12.567	21.369	22.682	1.00 38.81
ATOM	230	NE2	GLN A	A 289	9.288	24.683	20.141	1.00 37.72
ATOM	231	C	CINI	A 289	8.603	24.432	21.124	1.00 37.80
ATOM	232	0		A 290	9.519	25.935	19.744	1.00 38.28
ATOM	233 234	N CA		A 290	9.072	27.105	20.501	1.00 38.43
MOTA	235	CB		A 290	10.268	27.813	21.152	1.00 38.66
MOTA	236	CG		A 290	11.241	26.912	21.906	1.00 37.22
ATOM ATOM	237	CD1		A 290	12.438	26.540	21.332	1.00 35.94
ATOM	238	CE1		A 290	13.339	25.731	21.989	1.00 34.88
ATOM	239	CZ	TYR	A 290	13.061	25.293	23.244	1.00 35.86
ATOM	240	ОН	TYR	A 290	13.983	24.491	23.870	1.00 34.34
ATOM	241	CE2		A 290	11.872	25.660	23.866	1.00 36.55
ATOM	242	CD2		A 290	10.978	26.487	23.193	1.00 35.75
ATOM	243	C		A 290	8.329	28.158	19.650	1.00 39.65
MOTA	244	Ö	TYR	A 290	8.582	28.309	18.443	1.00 39.27
ATOM	245	N	LEU	A 291	7.443	28.924	20.296	1.00 40.18
ATOM	246	CA	LEU	A 291	6.740	29.985	19.611	1.00 40.92
ATOM	247	CB	LEU	A 291	5.444	30.367	20.327	1.00 41.69
ATOM	248	CG	LEU	A 291	4.371	29.301	20.591	1.00 43.47
ATOM	249	CD1	LEU	A 291	3.295	29.850	21.586	1.00 45.13
ATOM	250	CD2	LEU	A 291	3.716	28.890	19.300	1.00 43.40
ATOM	251	С	LEU	A 291	7.635	31.202	19.487	1.00 41.12
ATOM	252	0	LEU	A 291	8.382	31.554	20.393	1.00 40.66
MOTA	253	N	ARG	A 292	7.508	31.876	18.356	1.00 41.62
ATOM	254	CA	ARG	A 292	8.317	33.034	18.065	1.00 42.34
MOTA	255	CB	ARG	A 292	7.830	33.695	16.766	1.00 42.90
MOTA	256	CG	ARG	A 292	8.712	34.814	16.241	1.00 45.07
ATOM	257	CD	ARG	A 292	10.053	34.331	15.752	1.00 48.94 1.00 50.47
MOTA	258	NE	ARG	A 292	10.873	35.373	15.134	1.00 50.47
MOTA	259	CZ	ARG	A 292	10.786	35.746	13.871 13.051	1.00 55.75
MOTA	260	NHI	LARG	A 292	9.874	35.206 36.684	13.420	1.00 55.53
MOTA	261		ARG		11.605 8.206	34.005	19.199	1.00 33.33
ATOM	262	С	AKG	A 292	0.200	54.005		

ORENDED DE LA COLOCACIO DE LA C

ATOM	263	O A	RG A 2	292	9.213	34.496	19.732	1.00 41	
ATOM	264	N G	LU A 2	293	6.958	34.287	19.564	1.00 43	
ATOM	265		LU A 2		6.675	35.284	20.586	1.00 43	
ATOM	266		LU A 2		5.164	35.519	20.679	1.00 44	
ATOM	267		LU A 2		4.562	36.144	19.410	1.00 47 1.00 51	
ATOM	268		LU A 2		4.517	35.201	18.194	1.00 52	
ATOM	269		LU A 2		4.477	33.955	18.392	1.00 52	
MOTA	270		LU A		4.516	35.711	17.033	1.00 43	2.22
MOTA	271		SLU A 2		7.299	34.887	21.928	1.00 43	
ATOM	272	O G	LU A	293	7.878	35.732	22.598 22.303	1.00 43	
MOTA	273	M G	LU A	294	7.207	33.613	23.522	1.00 42	
MOTA	274		LU A		7.870	33.111 31.564	23.632	1.00 43	
MOTA	275	CB G	LU A	294	7.845 6.544	30.813	23.909	1.00 4	
MOTA	276		LU A			29.398	23.262	1.00 4	
ATOM	277		SLU A		6.529 7.355	28.479	23.591	1.00 42	
ATOM	278	OE1 G	SLU A	29 4	5.666	29.204	22.369	1.00 5	
MOTA	279		SLU A		9.364	33.469	23.488	1.00 4	
ATOM	280	_	GLU A : GLU A :		9.919	33.993	24.447	1.00 4	
ATOM	281		LEU A		10.017	33.106	22.388	1.00 3	
MOTA	282 283		LEU A		11.462	33.297	22.239	1.00 3	8.55
MOTA	284	CB I	LEU A	295	11.959	32.681	20.918	1.00 3	
MOTA	285	CG I	LEU A	295	11.815	31.163	20.806	1.00 3	8.68
ATOM ATOM	286	כס ז	LEU A	295	11.654	30.733	19.372	1.00 4	0.29
ATOM	287	CD2 I	LEU A	295	13.003	30.450	21.445	1.00 3	
ATOM	288	C	LEU A	295	11.866	34.759	22.318	1.00 3	
ATOM	289	0 1	LEU A	295	12.884	35.075	22.907	1.00 3	
ATOM	290	N (GLN A	296	11.052	35.640	21.749	1.00 3	
MOTA	291	CA (GLN A	296	11.323	37.083	21.755	1.00 3	
ATOM	292	CB (GLN A	296	10.390	37.802	20.775	1.00 3	9.49
ATOM	293		GLN A		10.709	37.498	19.284	1.00 4	3.93
ATOM	294		GLN A		9.671	38.037	18.263	1.00 4	
ATOM	295	OE1	GLN A	296	8.471	38.104	18.537	1.00 5 1.00 4	
MOTA	296	NE2	GLN A	296	10.152	38.397	17.079	1.00 4	
ATOM	297	C (GLN A	296	11.203	37,728	23.148 23.461	1.00 3	
MOTA	298	0	GLN A	296	11.898	38.696	23.401	1.00 3	
MOTA	299	N	GLN A	297	10.351 10.104	37.176 37.771	25.297	1.00 3	
MOTA	300		GLN A GLN A		8.692	37.402	25.783	1.00 3	
MOTA	301		GLN A		7.621	38.365	25.195	1.00 4	
MOTA	302 303		GLN A		6.170	37.850	25.288	1.00 4	
MOTA	304		GLN A		5.797	37.151	26.239	1.00 5	0.31
MOTA MOTA	305	NE2	GLN A	297	5.356	38.199	24.289	1.00 5	
ATOM	306	C	GLN A	297	11.177	37.428	26.347	1.00 3	
ATOM	307		GLN A		11.210	38.040	27.413	1.00 3	
ATOM	308		ILE A		12.045	36.452	26.059	1.00 3	
ATOM	309	CA	ILE A	298	13.087		27.007	1.00 3	
ATOM	310	CB	ILE A	298	12.920	34.651	27.472	1.00 3	4.23
ATOM	311	CG1	ILE A	298	12.999	33.705	26.282	1.00 3	
ATOM	312	CD1	ILE A	298	13.013	32.277	26.693	1.00 3 1.00 3	
ATOM	313		ILE A		11.588	34.413	28.205 26.479	1.00 3	
MOTA	314		ILE A		14.520	36.278	26.959	1.00 3	
MOTA	315	0	ILE A	298	15.421	35.612	25.518	1.00 3	2.43
MOTA	316		THR A		14.748	37.175 37.434	25.027	1.00 3	
MOTA	317	CA	THR A	299 200	16.110 16.149	38.398	23.832	1.00 3	
MOTA	318		THR A		15.244	39.478	24.047	1.00 3	
MOTA	319	OGT	THR A	299	15.653	37.762	22.528	1.00 3	
MOTA	320	CG2	THR A	299	17.000	38.007	26.104	1.00 3	
MOTA	321 322	С 0	THR A	299	18.212	37.917	26.015	1.00 3	
ATOM	323	И	TRP A	300	16.412	38.607	27.132	1.00 3	30.79
ATOM ATOM	324		TRP A		17.218	39.162	28.237	1.00 2	
ATOM	325	CB	TRP A		16.413	40.155	29.094	1.00 2	
ATOM	326	CG	TRP A	300	15.189	39.547	29.664	1.00 2	
ATOM	327	CD1	TRP A	300	13.988	39.423	29.044	1.00 2	
MOTA	328	NE1	TRP A	300	13.096	38.775	29.862	1.00 2	44.08

окороновороно

								1 00 04 03
ATOM	329	CE2	TRP A	300	13.727	38.462	31.033	1.00 24.93
ATOM	330	CD2	TRP A	300	15.045	38.926	30.936	1.00 23.62
ATOM	331	CE3	TRP A	300	15.884	38.761	32.030	1.00 26.31
ATOM	332		TRP A		15.415	38.153	33.128	1.00 27.39
ATOM	333		TRP A		14.083	37.700	33.201	1.00 28.78
			TRP A		13.231	37.857	32.168	1.00 24.74
MOTA	334				17.803	38.099	29.155	1.00 29.45
MOTA	335	С	TRP A			38.365	29.906	1.00 30.38
MOTA	336	0	TRP A		18.751			1.00 29.27
ATOM	337	N	GLN A		17.231	36.897	29.103	
ATOM	338	CA	GLN A		17.695	35.781	29.923	
ATOM	339	CB	GLN A		16.616	34.701	30.038	1.00 28.84
ATOM	340	CG	GLN A	301	15.419	35.171	30.791	1.00 30.22
ATOM	341	CD	GLN A		14.251	34.170	30.897	1.00 33.05
ATOM	342		GLN A		14.340	33.032	30.464	1.00 32.79
ATOM	343	NE2		301	13.144	34.633	31.479	1.00 34.45
		C	GLN A		18.964	35.186	29.327	1.00 29.50
ATOM	344		GLN A		18.926	34.117	28.725	1.00 30.22
ATOM	345	0			20.081	35.884	29.484	1.00 29.33
MOTA	346	N	THR A		21.372	35.407	29.007	1.00 29.03
MOTA	347	CA	THR A			36.588	28.567	1.00 29.13
MOTA	348	CB	THR A		22.271		29.603	1.00 28.27
MOTA	349	OG1			22.307	37.572		
MOTA	350	CG2	THR A		21.695	37.317	27.362	1.00 29.18
ATOM	351	С	THR A	302	22.024	34.662	30.165	1.00 29.23
ATOM	352	0	THR A		21.615	34.836	31.308	1.00 29.31
ATOM	353	N	PHE A		22.987	33.791	29.874	1.00 29.05
ATOM	354	CA	PHE A		23.704	33.101	30.929	1.00 29.57
	355	CB	PHE A		24.678	32.033	30.380	1.00 29.12
ATOM		CG	PHE A		23.998	30.815	29.837	1.00 27.07
ATOM	356		PHE A		23.798	30.691	28.475	1.00 27.05
ATOM	357	CD1			23.156	29.630	27.957	1.00 27.11
MOTA	358	CE1			22.699	28.639	28.795	1.00 27.76
ATOM	359	CZ	PHE A			28.746	30.156	1.00 27.13
MOTA	360	CE2	PHE A		22.884		30.669	1.00 26.38
MOTA	361	CD2			23.530	29.833		
ATOM	362	С	PHE A		24.461	34.134	31.780	
ATOM	363	0	PHE A		24.913	35.153	31.291	1.00 30.40
MOTA	364	N	LEU A		24.598	33.854	33.053	1.00 31.25
ATOM	365	CA	LEU A	304	25.332	34.733	33.954	1.00 32.65
ATOM	366	CB	LEU A	304	24.930	34.475	35.390	1.00 32.80
ATOM	367	CG	LEU A	304	23.457	34.647	35.722	1.00 33.60
ATOM	368	CD1			23.213	34.101	37.076	1.00 35.11
ATOM	369	CD2			23.051	36.084	35.695	1.00 35.33
ATOM	370	C	LEU A		26.800	34.424	33.797	1.00 34.30
	371	ŏ	LEU A		27.171	33.345	33.332	1.00 32.86
ATOM		N	GLN A		27.647	35.360	34.195	1.00 36.15
ATOM	372		GLN A		29.077	35.180	34.006	1.00 38.54
ATOM	373	CA	GLN A		29.852	36.381	34.584	1.00 39.68
ATOM	374	CB			31.293	36.596	34.029	1.00 42.48
MOTA	375	CG	GLN A		31.436	36.533	32.488	1.00 46.39
ATOM	376	CD	GLN A			37.118	31.720	1.00 46.08
MOTA	377	OE1			30.636			1.00 48.27
MOTA	378	NE2			32.497	35.850	32.041	
ATOM	379	С	GLN A		29.584	33.832	34.575	
MOTA	380	0	GLN A		30.428	33.194	33.968	1.00 39.34
MOTA	381	N	GLU A	306	29.031	33.391	35.698	1.00 39.71
ATOM	382	CA	GLU A		29.451	32.155	36.350	1.00 39.99
ATOM	383	CB	GLU A		28.756	31.992	37.705	1.00 41.15
ATOM	384	CG	GLU A		29.089	33.078	38.735	1.00 47.39
ATOM	385	CD	GLU A		28.167	33.080	39.980	1.00 55.43
	386	OE1			27.643	31.999	40.357	1.00 59.46
ATOM					27.962	34.167	40.612	1.00 60.68
ATOM	387	OE2		306	29.132	30.952	35.472	1.00 38.37
ATOM	388	C			29.132	30.022	35.353	1.00 38.01
ATOM	389	0	GLU A	306		30.022	34.889	1.00 36.34
ATOM	390	N	GTO Y	307	27.943		33.988	1.00 34.63
ATOM	391	CA	GLU A	A 307	27.514	29.927	33.5642	1.00 35.14
ATOM	392	CB		A 307	26.032	30.117	34.823	1.00 33.14
MOTA	393	CG		307	25.062	30.047		1.00 34.93
MOTA	394	CD	GLU A	A 307	23.620	30.319	34.412	T.00 JO.TO

 σ

- 72 -

Ö
С
N O
C
000
C
C
N
C
\sim
0000
00001
C
N
CCCO
C
0
N
ŏ
CONC
CCC
C
С
0000
C
C
C O
N
C
Č
C
CCCONC
_
N O
C
C
0
N C
o
N
C
С
C
N
С

0

1.00 36.82 1.00 32.29 29.382 34.543 OE1 GLU A 307 22.785 395 MOTA 23.312 28.395 28.752 33.946 31.467 OE2 GLU A 307 396 MOTA 1.00 33.42 32.716 29.957 GLU A 307 397 MOTA 1.00 30.28 28.907 32.177 GLU A 307 ILE A 308 398 0 MOTA 1.00 32.73 1.00 33.52 1.00 33.62 31.149 31.251 32.701 32.264 28.778 MOTA 399 N 29.593 29.723 28.384 31.062 400 CA **ILE A 308** MOTA 30.595 **ILE A 308** 401 CB MOTA 30.061 1.00 34.47 CG1 ILE A 308 CD1 ILE A 308 33.198 402 MOTA 1.00 34.55 28.385 34.618 29.697 403 MOTA 1.00 33.46 1.00 34.15 1.00 33.82 29.484 30.758 32.864 ILE A 308 CG2 MOTA 404 30.564 29.709 31.324 30.560 30.933 **ILE A 308** 405 С MOTA 31.373 31.549 ILE A 308 406 0 MOTA 30.899 32.447 1.00 35.66 GLU A 309 GLU A 309 407 N MOTA 32.858 34.199 34.048 1.00 36.34 32.813 30.284 408 CA MOTA 1.00 37.37 1.00 41.64 33.280 33.860 33.687 30.879 **GLU A 309** 409 CB MOTA 32.290 33.171 GLU A 309 GLU A 309 GLU A 309 GLU A 309 410 CG MOTA 35.295 1.00 46.42 CD MOTA 411 36.387 1.00 49.14 33.419 32.615 OE1 412 MOTA 1.00 51.22 1.00 35.17 35.174 34.426 33.805 OE2 MOTA 413 32.718 33.580 31.679 32.941 32.431 28.766 **GLU A 309** 414 С MOTA 1.00 35.55 GLU A 309 ASN A 310 ASN A 310 28.072 415 0 MOTA 28.249 33.578 1.00 34.21 416 N ATOM 33.603 1.00 34.07 31.478 26.817 417 418 CA ATOM 26.511 25.036 24.260 30.168 29.871 34.282 34.346 1.00 35.39 1.00 38.20 ASN A 310 CB MOTA CG ASN A 310 OD1 ASN A 310 ND2 ASN A 310 419 ATOM 1.00 45.99 34.994 30.608 MOTA 420 28.778 24.629 33.712 1.00 42.62 421 422 MOTA 26.202 25.193 26.795 1.00 33.34 1.00 33.73 32.212 31.488 32.171 ASN A 310 ATOM С 31.987 31.247 423 0 **ASN A 310** MOTA 1.00 31.41 30.780 30.793 TYR A 311 424 N ATOM 26.215 29.919 1.00 30.92 TYR A 311 TYR A 311 425 CA MOTA 1.00 30.60 1.00 29.73 28.959 26.904 26.519 29.821 426 CB MOTA 28.362 27.421 26.090 25.671 29.117 TYR A 311 427 CG ATOM 1.00 28.73 27.465 27.149 29.445 CD1 TYR A 311 428 ATOM 1.00 29.50 29.590 CE1 TYR A 311 CZ TYR A 311 429 ATOM 1.00 29.74 25.875 29.403 ATOM 430 1.00 32.23 1.00 29.37 24.332 26.578 27.925 32.192 25.610 29.557 TYR A 311 431 MOTA OH 24.897 25.224 29.056 432 CE2 TYR A 311 MOTA 1.00 29.13 28.915 CD2 TYR A 311 MOTA 433 1.00 31.46 26.310 29.367 TYR A 311 TYR A 311 C O 434 MOTA 1.00 30.86 25.434 27.398 27.554 32.635 32.890 28.636 435 MOTA 32.56 29.688 1.00 **GLN A 312** 436 N MOTA 34.251 34.706 29.209 1.00 33.54 GLN A 312 ATOM 437 CA 29.010 29.300 1.00 33.50 GLN A 312 GLN A 312 CB 438 MOTA 1.00 33.49 29.859 28.239 34.082 MOTA 439 CG 28.461 1.00 34.18 1.00 35.47 34.392 31.302 440 **GLN A 312** CD MOTA 31.667 32.127 34.841 29.542 OE1 GLN A 312 441 MOTA NE2 GLN A 312 C GLN A 312 O GLN A 312 27.449 1.00 31.68 34.172 35.202 442 MOTA 1.00 34.41 26.603 29.928 443 ATOM 1.00 34.43 26.270 26.151 25.192 36.250 34.834 29.394 MOTA 444 1.00 35.17 ASN A 313 ASN A 313 ASN A 313 31.116 445 N MOTA 31.827 1.00 36.70 35.680 MOTA 446 CA 35.383 25.209 33.333 1.00 37.66 447 CB MOTA 1.00 41.22 34.051 35.992 26.423 **ASN A 313** 448 CG MOTA 33.522 35.265 36.882 27.096 1.00 42.54 OD1 ASN A 313 449 ATOM 1.00 44.69 26.717 23.745 35.478 35.531 450 ND2 ASN A 313 MOTA ASN A 313 ASN A 313 31.310 1.00 36.84 451 С MOTA 1.00 36.22 1.00 36.29 36.405 22.889 31.568 452 0 MOTA 30.619 23.459 LYS A 314 34.412 ATOM 453 N 34.166 32.761 1.00 35.35 22.111 30.110 454 455 LYS A 314 CA MOTA 1.00 35.14 29.527 LYS A 314 LYS A 314 21.940 ATOM CB 22.032 30.526 1.00 35.45 31.628 456 CG MOTA 29.787 1.00 38.14 21.978 LYS A 314 30.290 MOTA 457 CD 1.00 39.70 22.009 30.733 LYS A 314 29.085 458 CE ATOM 1.00 44.38 29.206 35.186 31.917 21.049 LYS A 314 MOTA 459 NZ21.752 29.052 1.00 35.29 LYS A 314 460 C ATOM

ATOM	461	0		A 314	35.676	22.605	28.307	1.00 35.12 1.00 34.85
MOTA	462	N	GLN :	A 315	35.484	20.452 19.906	29.000 28.048	1.00 34.64
MOTA	463	CA	GLN .	A 315	36.430 36.771	18.469	28.417	1.00 34.90
MOTA	464	CB	GLN .	A 315	37.502	18.260	29.733	1.00 39.29
MOTA	465	CG	GLN .	A 315 A 315	38.919	18.804	29.697	1.00 44.94
ATOM	466	CD	GLM .	A 315	39.685	18.490	28.787	1.00 50.63
ATOM	467	OE1 NE2	GLM .	A 315	39.264	19.634	30.677	1.00 47.61
MOTA	468 469	C	GLM GLM	A 315	35.846	19.884	26.647	1.00 33.86
MOTA MOTA	470	Ö	GLN	A 315	34.631	19.748	26.460	1.00 32.99
ATOM	471	Ŋ		A 316	36.729	19.965	25.664	1.00 32.95
ATOM	472	CA		A 316	36.315	19.977	24.292	1.00 32.86
ATOM	473	CB		A 316	37.519	19.829	23.385	1.00 33.76 1.00 38.32
ATOM	474	CG	ARG	A 316	37.205	20.195	21.947 21.047	1.00 33.32
ATOM	475	CD		A 316	38.414	20.275 20.301	19.640	1.00 49.79
MOTA	476	NE		A 316	38.022 38.804	19.922	18.624	1.00 53.81
ATOM	477	CZ		A 316	40.036	19.479	18.847	1.00 55.22
ATOM	478	NH2	ARG	A 316 A 316	38.347	19.990	17.381	1.00 55.07
MOTA	479 480	C	ARG	A 316	35.289	18.895	23.966	1.00 31.22
ATOM ATOM	481	ŏ	ARG	A 316	34.241	19.187	23.405	1.00 28.96
ATOM	482	Ň	GLU	A 317	35.575	17.649	24.327	1.00 30.76
MOTA	483	CA	GLU	A 317	34.680	16.574	23.930	1.00 30.63
ATOM	484	CB	GLU	A 317	35.315	15.181	24.082 25.484	1.00 31.32 1.00 33.23
MOTA	485	CG	GLU	A 317	35.547	14.697 15.194	26.090	1.00 33.23
MOTA	486	CD	GLU	A 317	36.850 37.349	13.194 14.502	27.024	1.00 44.77
MOTA	487		GLU	A 317	37.345	16.259	25.674	1.00 34.98
ATOM	488	OE2	GLU	A 317 A 317	33.351	16.695	24.640	1.00 29.33
MOTA	489 490	C O		A 317	32.344	16.314	24.099	1.00 30.11
ATOM ATOM	491	N		A 318	33.365	17.256	25.829	1.00 27.92
ATOM	492	CA		A 318	32.173	17.464	26.628	1.00 27.86
ATOM	493	CB		A 318	32.529	17.835	28.082	1.00 28.20
ATOM	494	CG1	VAL	A 318	31.275	18.177	28.870	1.00 28.77 1.00 29.97
ATOM	495	CG2	VAL	A 318	33.263	16.646	28.741 26.013	1.00 27.21
MOTA	496	C		A 318	31.244 30.048	18.528 18.287	25.886	1.00 26.50
MOTA	497	0		A 318	30.048	19.670	25.603	1.00 26.29
ATOM	498	N	MEA	A 319 A 319	31.018	20.716	24.961	1.00 26.24
ATOM	499 500	CA CB	MET	A 319	31.852	22.004	24.831	1.00 27.30
ATOM ATOM	501	CG		A 319	31.050	23.268	24.597	1.00 28.90
ATOM	502	SD	MET	A 319	29.794	23.654	25.828	1.00 33.36
ATOM	503	CE	MET	A 319	28.848	24.807	24.932	1.00 31.15 1.00 25.53
ATOM	504	C		A 319	30.472	20.228	23.615 23.281	1.00 25.99
ATOM	505	0	MET		29.325	20.447 19.511	22.857	1.00 25.05
MOTA	506	N		A 320	31.267 30.790		21.621	1.00 24.82
MOTA	507	CA	TKP	A 320 A 320	31.923	18.183	20.921	1.00 24.80
ATOM	508 509	CB CG	TRE	A 320	32.634	18.949	19.867	1.00 27.31
MOTA MOTA	510	CD:		A 320	33.705	19.786	20.039	1.00 30.43
ATOM	511	NE		A 320	34.100	20.301	18.831	1.00 31.02
ATOM	512	CE		A 320	33.268	19.826	17.854	1.00 28.25
ATOM	513	CD	2 TRP	A 320	32.338	18.969	18.470	1.00 28.17 1.00 29.23
MOTA	514	CE		A 320	31.357	18.366	17.675 16.320	1.00 29.23
ATOM	515			A 320	31.356 32.293	18.606 19.478	15.739	1.00 28.19
MOTA	516			A 320			16.492	1.00 28.61
MOTA	517		Z TRE	A 320 A 320	33.260 29.594		21.832	1.00 24.11
MOTA	518		TKE	A 320	28.638		21.080	1.00 23.54
ATOM	519 520		C1'Y.	7 A 321	29.644		22.832	1.00 24.43
MOTA MOTA	521		GIN	J A 321	28.544	16.178	23.043	1.00 24.39
ATOM	522			1 A 321	28.836	15.179	24.168	
MOTA	523		GLI	1 A 321	27.876		24.140	
ATOM	524	CD		J A 321	27.120			
MOTA	525		1 GLN	V A 321	27.146			
MOTA	526	NE	Z GLI	N A 321	26.444	14.04/	23.930	

					02 250	1.00 24.19
ATOM	527 C	GLN A 321	27.249	16.900	23.359	1.00 24.19
ATOM	528 O	GLN A 321	26.180	16.559	22.832	1.00 24.08
ATOM	529 N	LEU A 322	27.368	17.924	24.178	
ATOM	530 CA		26.236	18.733	24.579	1.00 25.69
ATOM	531 CE		26.644	19.732	25.683	1.00 26.07
ATOM	532 CG		25.622	20.738	26.235	1.00 27.41
ATOM	533 CE	1 LEU A 322	24.406	20.074	26.909	1.00 29.40
ATOM	534 CI	2 LEU A 322	26.277	21.639	27.190	1.00 30.22
ATOM	535 C	LEU A 322	25.615	19.430	23.374	1.00 26.06
ATOM	536 0	LEU A 322	24.406	19.285	23.125	1.00 26.90
ATOM	537 N	CYS A 323	26.420	20.140	22.587	1.00 25.58 1.00 25.11
ATOM	538 CF	CYS A 323	25.893	20.774	21.384	
ATOM	539 CE	3 CYS A 323	26.996	21.554	20.686	1.00 25.72 1.00 29.20
ATOM	540 SC	CYS A 323	27.607	22.944	21.675	1.00 25.20
ATOM	541 C	CYS A 323	25.246	19.776	20.419	1.00 23.70
ATOM	542 O	CYS A 323	24.215	20.057	19.816	1.00 24.13
MOTA	543 N	ALA A 324	25.846	18.604	20.272 19.398	1.00 23.43
ATOM	544 C	A ALA A 324	25.275	17.625	19.222	1.00 24.05
MOTA	545 CI	B ALA A 324	26.226	16.462	19.222	1.00 23.43
MOTA	546 C	ALA A 324	23.913	17.141 16.938	19.125	1.00 22.57
MOTA	547 O	ALA A 324	23.011	16.932	21.218	1.00 23.59
MOTA	548 N		23.776 22.482	16.591	21.791	1.00 24.38
MOTA	549 C	A ILE A 325	22.556	16.407	23.323	1.00 24.71
MOTA	550 C		23.293	15.136	23.709	1.00 25.02
MOTA		G1 ILE A 325	23.649	15.149	25.190	1.00 27.28
MOTA		D1 ILE A 325	21.158	16.398	23.942	1.00 22.26
ATOM		G2 ILE A 325	21.479	17.705	21.501	1.00 24.86
MOTA	554 C		20.384	17.453	21.044	1.00 24.56
MOTA	555 O	006	21.856	18.940	21.772	1.00 25.56
MOTA	556 N 557 C		20.926	20.047	21.580	1.00 26.26
MOTA	557 C 558 C		21.489	21.318	22.184	1.00 26.21
ATOM ATOM	559 C		21.741	21.248	23.681	1.00 29.37
ATOM	560 C		20.479	20.914	24.433	1.00 33.36
ATOM		E LYS A 326	20.725	20.802	25.926	1.00 36.77
ATOM	562 N	Z LYS A 326	19.694	19.921	26.567	1.00 37.66
ATOM	563 C	LYS A 326	20.520	20.209	20.094	1.00 26.40 1.00 25.16
ATOM	564 O	LYS A 326	19.348	20.386	19.803	1.00 25.10
ATOM	565 N	ILE A 327	21.480	20.110	19.175 17.740	1.00 28.16
MOTA		A ILE A 327	21.208	20.174 20.235	16.930	1.00 29.15
MOTA		B ILE A 327	22.511	20.235	16.335	1.00 35.09
ATOM		G1 ILE A 327	22.666	21.810	15.538	1.00 39.84
MOTA		D1 ILE A 327	23.951 22.465	19.314	15.745	1.00 31.87
MOTA		G2 ILE A 327	20.378	19.015	17.250	1.00 27.66
MOTA	571 C		19.544	19.152	16.361	1.00 27.77
ATOM	572		20.599	17.855	17.811	1.00 27.88
ATOM	573 N		19.810	16.726	17.415	1.00 28.75
MOTA		CA THR A 328 CB THR A 328	20.328	15.479	18.028	1.00 29.15
ATOM		G1 THR A 328	21.665	15.267	17.581	1.00 28.97
ATOM ATOM		G2 THR A 328	19.547	14.287	17.518	1.00 30.09
ATOM		THR A 328	18.343	16.927	17.776	1.00 28.80
ATOM		THR A 328	17.496	16.567	16.986	1.00 27.42
MOTA		J GLU A 329	18.051	17.530	18.928	1.00 29.14
ATOM		CA GLU A 329	16.658	17.852	19.278	1.00 30.60
MOTA		CB GLU A 329	16.546	18.559	20.643	1.00 31.73
ATOM		CG GLU A 329	17.198	17.863	21.820	1.00 37.45 1.00 43.70
MOTA		CD GLU A 329	17.178	18.684	23.122	1.00 43.70
MOTA		DE1 GLU A 329	16.578	19.802	23.159	1.00 42.77
MOTA		DE2 GLU A 329	17.756	18.174	24.135 18.215	1.00 49.00
MOTA	-	GLU A 329	15.985		17.776	
MOTA		O GLU A 329	14.864 16.648		17.825	
ATOM		N ALA A 330	16.105		16.793	
MOTA		CA ALA A 330 CB ALA A 330	16.981		16.610	1.00 27.09
MOTA		CB ALA A 330 C ALA A 330	15.900		15.447	
ATOM	592	C AMIL A 300				

		14 011	20.208	14.753	1.00 27.51
MOTA	593 O ALA A 330		20.208 19.109	15.070	1.00 26.90
MOTA	594 N ILE A 331		18.308	13.860	1.00 27.25
ATOM	595 CA ILE A 331		17.520	13.585	1.00 26.89
MOTA	596 CB ILE A 331		18.507	13.149	1.00 27.96
MOTA	597 CG1 ILE A 331 598 CD1 ILE A 331		17.877	12.923	1.00 29.48
MOTA			16.414	12.484	1.00 26.39
MOTA	599 CG2 ILE A 331 600 C ILE A 331	15.470	17.390	13.885	1.00 27.69
ATOM			17.205	12.859	1.00 27.06
ATOM			16.830	15.041	1.00 28.59
MOTA	602 N GLN A 332 603 CA GLN A 332	13.987	15.988	15.167	1.00 30.50
ATOM ATOM	604 CB GLN A 332	13.849	15.439	16.579	1.00 31.71
ATOM	605 CG GLN A 332		14.109	16.681	1.00 36.53
ATOM	606 CD GLN A 332		13.693	18.084	1.00 43.18 1.00 46.43
ATOM	607 OE1 GLN A 332		14.274	19.043	1.00 46.43
ATOM	608 NE2 GLN A 332		12.680	18.228 14.763	1.00 30.16
ATOM	609 C GLN A 332	12.736	16.742 16.192	14.785	1.00 29.89
ATOM	610 O GLN A 332	11.879 12.666	18.012	15.142	1.00 29.91
MOTA	611 N TYR A 333	11.548	18.863	14.773	1.00 29.79
MOTA	612 CA TYR A 333 613 CB TYR A 333	11.552	20.152	15.632	1.00 30.02
MOTA		11.052	19.929	17.038	1.00 30.98
MOTA	614 CG TYR A 333 615 CD1 TYR A 333	11.928	19.789	18.095	1.00 32.18
MOTA MOTA	616 CE1 TYR A 333	11.460	19.555	19.372	1.00 34.65
ATOM	617 CZ TYR A 333	10.097	19.474	19.605	1.00 35.79
MOTA	618 OH TYR A 333	9.635	19.256	20.875	1.00 40.22
MOTA	619 CE2 TYR A 333	9.207	19.621	18.590	1.00 34.47
MOTA	620 CD2 TYR A 333	9.687	19.858	17.305	1.00 34.75 1.00 29.21
ATOM	621 C TYR A 333	11.543	19.187	13.272 12.658	1.00 29.48
MOTA	622 O TYR A 333	10.498	19.330 19.337	12.683	1.00 28.49
MOTA	623 N VAL A 334	12.711 12.781	19.602	11.247	1.00 28.13
MOTA	624 CA VAL A 334	14.204	20.060	10.872	1.00 28.00
MOTA	625 CB VAL A 334 626 CG1 VAL A 334	14.470	19.953	9.349	1.00 28.89
ATOM		14.441	21,427	11.401	1.00 26.70
MOTA	627 CG2 VAL A 334 628 C VAL A 334	12.347	18.349	10.439	1.00 27.92
MOTA MOTA	629 O VAL A 334	11.770	18.465	9.378	1.00 26.84
ATOM	630 N VAL A 335	12.612	17.158	10.948	1.00 28.87
ATOM	631 CA VAL A 335	12.151	15.943	10.276	1.00 30.06 1.00 30.00
MOTA	632 CB VAL A 335	12.737	14.699	10.894 10.339	1.00 30.00
ATOM	633 CG1 VAL A 335	12.072	13.487 14.592	10.533	1.00 32.37
MOTA	634 CG2 VAL A 335	14.210 10.588	15.881	10.266	1.00 30.90
ATOM	635 C VAL A 335	9.984	15.468	9.263	1.00 29.27
MOTA	636 O VAL A 335 637 N GLU A 336	9.953	16.356	11.344	1.00 31.20
ATOM		8.489	16.425	11.393	1.00 32.50
ATOM	638 CA GLU A 336 639 CB GLU A 336	7.961	16.735	12.812	1.00 33.25
MOTA MOTA	640 CG GLU A 336	8.283	15.671	13.862	1.00 36.91
ATOM	641 CD GLU A 336	7.627	14.299	13.616	1.00 44.18
ATOM	642 OE1 GLU A 336	6.463	14.240	13.123	1.00 48.70
MOTA	643 OE2 GLU A 336	8.276	13.256	13.928	1.00 47.83 1.00 31.88
ATOM	644 C GLU A 336	7.980	17.440	10.380 9.697	1.00 32.26
MOTA	645 O GLU A 336	6.994	17.194 18.569	10.246	1.00 31.25
MOTA	646 N PHE A 337	8.654 8.315	19.488	9.189	1.00 31.26
MOTA	647 CA PHE A 337	9.270	20.670	9.251	1.00 31.46
ATOM	648 CB PHE A 337 649 CG PHE A 337	9.017	21.746	8.229	1.00 30.00
MOTA		7.842	22.467	8.237	1.00 29.18
MOTA ATOM	650 CD1 PHE A 337 651 CE1 PHE A 337	7.643	23.484	7.357	1.00 29.25
MOTA	652 CZ PHE A 337	8.620	23.811	6.418	1.00 30.20
ATOM	653 CE2 PHE A 337	9.799	23.094	6.381	1.00 30.76
MOTA	654 CD2 PHE A 337	9.988	22.059	7.287	1.00 31.21 1.00 32.11
MOTA	655 C PHE A 337	8.364	18.826	7.779 7.011	
MOTA	656 O PHE A 337	7.402	18.929 18.176	7.438	
MOTA	657 N ALA A 338	9.479 9.618	17.536	6.134	
ATOM	658 CA ALA A 338	5.020			

						4.6 - 5.5	6 000	1 00 34 40
MOTA	659		ALA A		10.936	16.787	6.029	1.00 34.40
ATOM	660		ALA A		8.448	16.593	5.849	1.00 35.78
MOTA	661		ALA A		7.848	16.667	4.806	1.00 35.41
ATOM	662		LYS A		8.127	15.725	6.790	1.00 37.72
MOTA	663	CA	LYS A		7.058	14.776	6.598	1.00 39.80 1.00 40.02
MOTA	664	CB	LYS A	339	6.761	14.056	7.886	
ATOM	665	CG	LYS A	339	7.901	13.158	8.291	1.00 42.45
ATOM	666	CD	LYS A		7.440	11.942	9.028	1.00 44.60
ATOM	667	CE	LYS A		7.206	12.224	10.454	1.00 46.22
ATOM	668	NZ	LYS A	339	7.415	10.966	11.174	1.00 46:80
MOTA	669	С	LYS A	339	5.777	15.391	6.072	1.00 41.25
MOTA	670	0	LYS A		5.091	14.789	5.275	1.00 41.74
MOTA	671	N	ARG A		5.485	16.605	6.497	1.00 42.74
ATOM	672	CA	ARG A		4.266	17.275	6.127	1.00 43.70
ATOM	673	CB	ARG A	340	3.887	18.223	7.229	1.00 43.78
ATOM	674	CG	ARG A		3.550	17.533	8.494	1.00 45.03
ATOM	675	CD	ARG A		3.273	18.483	9.594	1.00 46.53
ATOM	676	NE	ARG A	340	3.333	17.821	10.887	1.00 49.07
ATOM	677	CZ	ARG A		2.578	18.165	11.915	1.00 51.42
ATOM	678	NH1	ARG A	340	1.697	19.167	11.779	1.00 53.86
ATOM	679	NH2	ARG A		2.691	17.510	13.063	1.00 50.56
ATOM	680	C	ARG A	340	4.355	18.086	4.858	1.00 44.39
ATOM	681	0	ARG A		3.381	18.710	4.473	1.00 44.75
ATOM	682	N	ILE A	341	5.516	18.136	4.231	1.00 44.93
ATOM	683	CA	ILE A	341	5.626	18.907	3.015	1.00 45.79
ATOM	684	CB	ILE A		7.073	19.340	2.776	1.00 45.44
ATOM	685	CG1	ILE A	341	7.446	20.384	3.818	1.00 45.69
ATOM	686	CD1	ILE A		8.901	20.710	3.847	1.00 46.77
ATOM	687	CG2	ILE A		7.240	19.881	1.357	1.00 45.67
ATOM	688	C	ILE A	341	5.080	18.035	1.895	1.00 46.85
ATOM	689	0	ILE A		5.483	16.883	1.738	1.00 46.56
MOTA	690	N	ASP A	342	4.148	18.593	1.129	1.00 48.25
ATOM	691	CA	ASP A	342	3.476	17.821	0.093	1.00 49.01
ATOM	692	CB	ASP A	342	2.306	18.611	-0.490	1.00 50.45
ATOM	693	CG	ASP A		1.152	<u>18.788</u>	0.493	1.00 53.95
ATOM	694	OD1	ASP A	342	0.695	17.786	1.084	1.00 58.87
ATOM	695	OD2	ASP A	342	0.636	19.914	0.713	1.00 59.55
ATOM	696	С	ASP A	342	4.424	17.453	-1.031	1.00 48.01
ATOM	697	0	ASP A		4.927	18.316	-1.747	1.00 47.92
ATOM	698	N	GLY A		4.642	16.155	-1.185	1.00 46.69
ATOM	699	CA	GLY A		5.544	15.642	-2.199	1.00 45.52
ATOM	700	C	GLY A		6.710	14.888	-1.596	1.00 43.87
ATOM	701	0	GLY A	343	7.268	13.970	-2.205	1.00 43.67
ATOM	702	N	PHE A	344	7.045	15.232	-0.365	1.00 41.81
ATOM	703	CA	PHE A	344	8.221	14.673	0.266	1.00 40.97
ATOM	704	CB	PHE A	344	8.588	15.453	1.533	1.00 40.64
MOTA	705	CG	PHE A		9.850	14.977	2.170	1.00 38.48
MOTA	706	CD1	PHE A	344	11.081	15.500	1.814	1.00 36.83
ATOM	707	CE1	PHE A	344	12.245	15.020	2.396	1.00 37.61
ATOM	708	CZ	PHE A	344	12.190	14.000	3.311	1.00 36.20
MOTA	709	CE2	PHE A	. 344	10.961	13.456	3.658	1.00 36.79
MOTA	710	CD2	PHE A	344	9.809	13.939	3.084	1.00 36.78
ATOM	711	С	PHE A	344	7.999	13.204	0.543	1.00 41.48
ATOM	712	0	PHE A	344	8.864	12.366	0.254	1.00 41.42
MOTA	713	N	MET A	345	6.814	12.881	1.056	1.00 42.09
ATOM	714	CA	MET A	345	6.447	11.536	1.370	1.00 43.10
ATOM	715	CB	MET A	345	5.247	11.496	2.326	1.00 43.84
ATOM	716	CG	MET A	345	5.590	11.871	3.775	1.00 46.08
ATOM	717	SD	MET A		7.102	11.080	4.441	1.00 50.98
ATOM	718	CE	MET A		6.721	9.279	4.354	1.00 52.61
ATOM	719	C	MET A	345	6.187	10.673	0.109	1.00 43.55
ATOM	720	Õ	MET A	345	6.190	9.427	0.184	1.00 42.43
ATOM	721	N	GLU A	346	5.974	11.311	-1.040	1.00 44.36
ATOM	722	CA	GLU A	346	5.839	10.568	-2.291	1.00 45.64
ATOM	723	CB	GLU A	346	5.107	11.384	-3.339	1.00 46.00
MOTA	724	CG	GLU A		3.616	11.455	-3.132	1.00 49.03
	. – –	-						

								1 00 54 25
ATOM	725		LU A		2.989	12.662	-3.821	1.00 54.25 1.00 56.30
MOTA	726		LU A		3.726	13.555	-4.328 -3.852	1.00 58.05
ATOM	727		LU A		1.740	12.718	-2.901	1.00 45.79
MOTA	728	C G	LU A	346	7.182	10.143 9.327	-3.826	1.00 46.33
MOTA	729		LU A		7.209	10.691	-2.411	1.00 45.30
ATOM	730		EU A		8.288	10.361	-2.983	1.00 44.95
MOTA	731		EU A		9.593	11.445	-2.650	1.00 44.65
MOTA	732		EU A		10.618 10.252	12.868	-3.077	1.00 44.22
MOTA	733	CG I	EU A	34/	11.065	13.905	-2.341	1.00 43.57
ATOM	734		EU A		10.447	13.049	-4.576	1.00 44.47
ATOM	735		LEU A		10.086	9.010	-2.469	1.00 44.60
ATOM	736		EU A		9.634	8.530	-1.426	1.00 43.99
ATOM	737		CYS A		11.007	8.392	-3.205	1.00 44.39
ATOM	738		CYS A		11.599	7.132	-2.754	1.00 44.78
MOTA	739 740		CYS A		12.511	6.526	-3.835	1.00 44.94
MOTA	740 741		CYS A		13.860	7.612	-4.385	1.00 48.13
ATOM	742		CYS A		12.388	7.401	-1.474	1.00 43.97
ATOM ATOM	743	ŏ	CYS A	348	12.982	8.475	-1.326	1.00 42.90
ATOM	744		GLN A		12.401	6.427	-0.567	1.00 43.70
ATOM	745		GLN A		13.096	6.569	0.708	1.00 44.41
ATOM	746		GLN A		13.178	5.250	1.487	1.00 45.15
ATOM	747		GLN A	349	13.587	5.479	2.949	1.00 47.77
ATOM	748	CD (GLN A	349	13.747	4.207	3.723	1.00 51.04
ATOM	749	OE1	GLN A	349	13.880	3.124	3.139	1.00 53.73 1.00 53.95
ATOM	750		GLN A		13.761	4.325	5.040	1.00 33.93
ATOM	751	C	GLN A	349	14.499	7.124	0.495	1.00 43.54
MOTA	752	0 (GLN A	349	15.017	7.862	1.324 -0.623	1.00 43.32
MOTA	753	N	ASN A	350	15.106	6.753 7.175	-0.023	1.00 43.26
ATOM	754		ASN A		16.451	6.460	-2.175	1.00 43.98
MOTA	755		ASN A		16.936 16.970	4.940	-1.994	1.00 48.26
MOTA	756	CG	ASN A	350	18.058	4.340	-1.904	1.00 52.77
ATOM	757		ASN A		15.773	4.305	-1.934	1.00 51.57
ATOM	758	ND2	ASN A ASN Ā	350	16.563	8.686	-1.116	1,00 40.98
ATOM	759		ASN A		17.499	9.296	-0.637	1.00 40.25
ATOM	760 761	N .	ASP A	350	15.638	9.266	-1.860	1.00 39.10
MOTA	762		ASP A		15.643	10.696	-2.065	1.00 38.32
ATOM ATOM	763		ASP A		14.794	11.100	-3.253	1.00 38.60
ATOM	764		ASP A		15.504	10.847	-4.590	1.00 41.32
ATOM	765		ASP A		16.656	10.309	-4.587	1.00 42.06
ATOM	766		ASP A		14.977	11.143	-5.686	1.00 42.98
ATOM	767	С	ASP A	351	15.194	11.404	-0.783	1.00 36.92
ATOM	768	0	ASP A	351	15.721	12.435	-0.464	1.00 35.52 1.00 35.97
ATOM	769	N	GLN A	352	14.279	10.813	-0.023	1.00 35.97 1.00 35.61
MOTA	770		GLN F		13.905	11.377	1.265 1.950	1.00 35.48
MOTA	771		GLN A		12.875	10.478 10.599	1.322	1.00 37.95
MOTA	772	CG	GLN A	352	11.497 10.561	9.498	1.737	1.00 40.62
MOTA	773	CD	GLN A	352	10.668	8.974	2.839	1.00 40.95
ATOM	774	OE1	GLN A	352	9.649	9.123	0.848	1.00 44.80
ATOM	775		GLN A	352	15.154	11.554	2.137	1.00 34.57
ATOM	776	C	GLN A	3 3 3 2 2	15.388	12.611	2.720	1.00 32.40
ATOM	777 778	O N	ILE A	3 353	15.970	10.508	2.184	1.00 33.88
MOTA MOTA	779		ILE A	A 353	17.178	10.487	3.002	1.00 34.01
ATOM	780		ILE A	A 353	17.772	9.049	2.998	1.00 33.98
ATOM	781			A 353	16.805	8.112	3.715	1.00 36.61
ATOM	782		ILE A		17.075	6.631	3.477	1.00 38.26
ATOM	783	CG2	ILE A	A 353	19.101	9.002	3.715	1.00 34.10
ATOM	784		ILE 2	A 353	18.225	11.498	2.548	1.00 32.99
ATOM	785		ILE A	A 353	18.821	12.187	3.364	1.00 32.18
MOTA	786		VAL 2	A 354	18.466	11.563	1.246	1.00 31.86 1.00 31.38
ATOM	787		VAL A	A 354	19.433	12.515	0.698	1.00 31.38
MOTA	788			A 354	19.569	12.320	-0.821 -1.458	1.00 31.30
MOTA	789		VAL	A 354	20.148 20.388	13.516 11.039	-1.149	1.00 32.45
MOTA	790	CG2	VAL .	A 334	20.300	11.009		

		_		. 251	10	.066	13.988	0.998	1.00 29.81
ATOM	791	C	VAL	A 354 A 354		.939	14.794	1.317	1.00 29.46
MOTA	792 793	N O		A 355		.780	14.316	0.901	1.00 28.52
ATOM ATOM	794	CA	LEU .	A 355	17	.317	15.673	1.175	1.00 27.57
ATOM	795	CB	LEU	A 355		.867	15.859	0.755	1.00 27.23
ATOM	796	CG	LEU	A 355		.593	15.830	-0.741	1.00 27.16
ATOM	797	CD1	LEU	A 355		.104	15.935	-0.931	1.00 28.72
ATOM	798	CD2	LEU	A 355		.337	16.878	-1.514	1.00 26.89 1.00 26.38
ATOM	799	C	LEU	A 355		.435	16.028	2.642	1.00 24.91
ATOM	800	0	LEU	A 355		7.724	17.171	2.969 3.522	1.00 24.31
MOTA	801	N		A 356		1.184	15.067 15.291	4.962	1.00 28.02
MOTA	802	CA		A 356		7.330 5.567	14.232	5.788	1.00 28.75
ATOM	803	CB		A 356 A 356		5.046	14.442	5.700	1.00 31.27
ATOM	804	CG	LEU	A 356		1.317	13.319	6.329	1.00 33.71
MOTA	805 806	CD1	LEU	A 356		1.608	15.740	6.323	1.00 31.98
ATOM ATOM	807	C	LEU	A 356	18	3.785	15.340	5.404	1.00 27.73
ATOM	808	ŏ	LEU	A 356	19	9.138	16.160	6.234	1.00 27.81
ATOM	809	N	LYS	A 357		9.631	14.463	4.891	1.00 28.00
ATOM	810	CA	LYS	A 357		L.038	14.523	5.263	1.00 29.47
ATOM	811	CB		A 357		1.875	13.426	4.613 5.037	1.00 29.39 1.00 33.92
MOTA	812	CG		A 357		1.562	12.033 11.034	4.457	1.00 33.32
ATOM	813	CD		A 357		2.586	9.804	5.331	1.00 41.03
MOTA	814	CE		A 357		2.683 3.255	8.598	4.607	1.00 43.01
MOTA	815	NZ	LVC	A 357 A 357		1.600	15.853	4.830	1.00 29.89
ATOM	816	C	TVC	A 357		2.382	16.444	5.542	1.00 30.98
ATOM	817 818	И	AT.A	A 358		1.207	16.338	3.657	1.00 30.12
ATOM ATOM	819	CA	ALA	A 358	2	1.750	17.612	3.181	1.00 30.98
ATOM	820	СВ		A 358	2	1.753	17.654	1.658	1.00 31.73
ATOM	821	C_	ALA	A 358		1.056	18.857	3.702	1.00 30.81
ATOM	822	0	ALA	A 358		1.686	19.893	3.875	1.00 33.30 1.00 29.32
MOTA	823	N	GLY	A 359	1	9.765	18.777	3.940 4.331	1.00 29.52
MOTA	824	CA		A 359	1	9.040	19.938 20.119	5.764	1.00 27.82
MOTA	825	C		A 359		8.606 8.236	21.223	6.110	1.00 27.60
ATOM	826	O	CED	A 359 A 360		8.630	19.089	6.591	1.00 26.28
ATOM	827 828	N CA	SER	A 360		8.064	19.239	7.905	1.00 26.79
ATOM ATOM	829	CB		A 360		7.984	17.889	8.631	1.00 27.01
ATOM	830	OG		A 360	1.	9.287	17.372	8.858	1.00 30.95
ATOM	831	C		A 360		8.786	20.315	8.699	1.00 26.61
ATOM	832	0		A 360		8.139	21.164	9.310	1.00 26.71 1.00 26.46
MOTA	833	N	LEU	A 361		0.116	20.345 21.373	8.635 9.338	1.00 26.75
MOTA	834	CA		A 361	2	0.887	21.373	9.306	1.00 26.79
MOTA	835	CB	LEU	A 361	2	3.250	21.762	10.334	1.00 28.75
ATOM	836	CG		A 361 A 361		2.803	21.528	11.780	1.00 28.83
MOTA	837 838	CD:	TIEU	A 361	_	4.747	21.342	10.154	1.00 30.56
MOTA MOTA	839	C.	LEU	A 361		0.660	22.765	8.782	1.00 26.67
ATOM	840	ŏ	LEU	A 361		0.593	23.740	9.545	1.00 26.63
ATOM	841	N	GLU	A 362		20.550	22.885	7.468	1.00 25.93
ATOM	842	CA		A 362		20.258	24.192	6.875	1.00 26.57 1.00 26.98
MOTA	843	CB	GLU	A 362		20.158	24.122	5.357 4.674	1.00 20.30
MOTA	844	CG	GLU	A 362		21.329 21.206	23.433 23.396	3.149	1.00 37.21
MOTA	845	CD	GLU	A 362		22.086		2.478	1.00 41.59
ATOM	846	OE	T GTI	TA 362		20.212		2.619	1.00 43.73
MOTA	847	C	∠ GDU (27.1)	J A 362 J A 362		18.931		7.430	1.00 25.89
MOTA	848 849		GI'I.	J A 362		18.823		7.697	1.00 24.74
MOTA MOTA	850		VAI	A 363		17.920	23.868	7.592	1.00 25.19
ATOM	851			A 363		16.647	24.362	8.112	1.00 26.09
ATOM	852	CB	VAI	A 363		15.494		7.990	1.00 25.99 1.00 27.49
ATOM	853	CG	1 VAI	A 363		14.256		8.658	1.00 27.49
MOTA	854		2 VAI	A 363		15.182		6.538 9.574	
ATOM	855			A 363		16.815 16.210		10.020	4 00 05 45
MOTA	856	0	VAL	A 363	•	-0.210	23.752		

a mont	857	N VAL A 364	17.682	24.091	10.308	1.00 26.29
MOTA MOTA	858	CA VAL A 364	17.942	24.451	11.690	1.00 25.82
MOTA	859	CB VAL A 364	18.867	23.435	12.363 13.716	1.00 26.43 1.00 25.43
MOTA	860	CG1 VAL A 364	19.315	23.910 22.105	12.538	1.00 27.04
MOTA	861	CG2 VAL A 364	18.171 18.528	25.865	11.747	1.00 26.05
MOTA	862	C VAL A 364 O VAL A 364	18.110	26.692	12.570	1.00 25.23
MOTA	863	O VAL A 364 N PHE A 365	19.491	26.162	10.877	1.00 25.43
ATOM ATOM	864 865	CA PHE A 365	20.098	27.491	10.897	1.00 25.79
MOTA	866	CB PHE A 365	21.372	27.506	10.102	1.00 26.05
ATOM	867	CG PHE A 365	22.482	26.755	10.743	1.00 26.79
ATOM	868	CD1 PHE A 365	22.830	26.990	12.046	1.00 28.32 1.00 29.90
ATOM	869	CE1 PHE A 365	23.869	26.329 25.430	12.628 11.894	1.00 23.30
ATOM	870	CZ PHE A 365	24.601 24.290	25.215	10.614	1.00 30.47
ATOM	871	CE2 PHE A 365 CD2 PHE A 365	23.226	25.886	10.024	1.00 29.26
ATOM ATOM	872 873	C PHE A 365	19.157	28.591	10.418	1.00 26.05
ATOM	874	O PHE A 365	19.265	29.745	10.846	1.00 26.08
ATOM	875	N ILE A 366	18.213	28.242	9.554	1.00 26.60
ATOM	876	CA ILE A 366	17.183	29.194	9.178 7.970	1.00 27.03 1.00 27.55
ATOM	877	CB ILE A 366	16.365 17.273	28.719 28.657	6.731	1.00 27.31
ATOM	878	CG1 ILE A 366 CD1 ILE A 366	16.641	28.018	5.520	1.00 26.80
MOTA	879 880	CD1 ILE A 366 CG2 ILE A 366	15.179	29.670	7.720	1.00 27.78
ATOM ATOM	881	C ILE A 366	16.325	29.422	10.404	1.00 26.64
ATOM	882	O ILE A 366	16.186	30.523	10.833	1.00 27.09
MOTA	883	N ARG A 367	15.792	28.375	11.009	1.00 27.45 1.00 27.84
ATOM	884	CA ARG A 367	14.990	28.542 27.204	12.229 12.733	1.00 27.84
MOTA	885	CB ARG A 367	14.500 13.501	26.572	11.840	1.00 27.21
ATOM	886	CG ARG A 367 CD ARG A 367	12.989	25.262	12.377	1.00 26.26
MOTA	887 888	CD ARG A 367 NE ARG A 367	11.797	24.825	11.687	1.00 27.92
ATOM ATOM	889	CZ ARG A 367	11.017	23.827	12.095	1.00 30.29
MOTA	890	NH1 ARG A 367	11.308	23.140	13.190	1.00 30.75 1.00 31.09
ATOM	891	NH2 ARG A 367	9.933	23.529	11.412 13.367	1.00 28.32
MOTA	892	C ARG A 367	15.723 15.104	29.268 29.904	14.228	1.00 28.51
ATOM	893	O ARG A 367 N MET A 368	17.038	29.172	13.374	1.00 29.28
ATOM ATOM	894 895	N MET A 368 CA MET A 368	17.832	29.887	14.359	1.00 30.61
ATOM	896	CB MET A 368	19.311	29.754	14.039	1.00 30.32
ATOM	897	CG MET A 368	20.188	30.279	15.100	1.00 30.51 1.00 31.75
ATOM	898	SD MET A 368	21.905	29.966	14.792 13.388	1.00 31.75 1.00 33.23
MOTA	899	CE MET A 368	22.107 17.484	30.986 31.372	14.427	1.00 33.23
ATOM	900	C MET A 368 O MET A 368	17.590	31.982	15.481	1.00 31.35
ATOM	901 902	O MET A 368 N CYS A 369	17.074	31.963	13.328	1.00 32.36
ATOM ATOM	903	CA CYS A 369	16.775	33.385	13.375	1.00 34.85
ATOM	904	CB CYS A 369	16.614	34.005	11.987	1.00 35.08
ATOM	905	SG CYS A 369	15.048	33.719	11.195 14.286	1.00 41.49 1.00 34.66
MOTA	906		15.601 15.556	33.738 34.844	14.785	1.00 36.34
MOTA	907		14.705	32.794	14.569	1.00 33.99
MOTA	908 909		13.589	33.045	15.460	1.00 32.77
MOTA ATOM	910		12.559	31.933	15.319	1.00 32.42
ATOM	911	CG ARG A 370	12.173	31.608	13.890	1.00 32.81
ATOM	912	CD ARG A 370	11.507	30.270	13.790	1.00 33.89 1.00 32.17
MOTA	913		10.153 9.752	30.290 29.738	14.304 15.412	1.00 32.17
ATOM	914		10.598	29.738	16.193	1.00 35.61
MOTA	915 916		8.472	29.815	15.748	1.00 33.49
ATOM ATOM	917		14.051	33.036	16.912	1.00 32.83
MOTA	918	O ARG A 370	13.322	33.465	17.817	1.00 32.92
ATOM	919	N ALA A 371	15.241	32.488	17.131	1.00 31.07 1.00 29.60
MOTA	920		15.757 15.928		18.455 18.720	1.00 29.76
MOTA	921		17.077		18.554	1.00 28.59
MOTA	922	C ALA A 371	_,,			

ATOM	923	0	ALA A	371	17.964	32.561	19.226	1.00 27.57
ATOM	924	N	PHE A		17.198	34.127	17.888 17.848	1.00 28.91 1.00 28.90
ATOM	925	CA	PHE A		18.452	34.836	16.480	1.00 28.04
ATOM	926	CB	PHE A		19.079	34.660 35.112	16.406	1.00 27.18
MOTA	927	CG	PHE A	372	20.485	34.231	16.614	1.00 28.47
MOTA	928	CD1	PHE A	3/2	21.515 22.829	34.661	16.546	1.00 30.76
MOTA	929		PHE A		23.107	36.004	16.312	1.00 28.92
MOTA	930	CZ	PHE A	372	22.085	36.873	16.119	1.00 28.65
ATOM	931	CE2 CD2	PHE A	372	20.781	36.429	16.158	1.00 27.09
ATOM	932 933	CDZ	PHE A		18.202	36.304	18.127	1.00 30.17
ATOM	934	Ö	PHE A		17.312	36.889	17.543	1.00 30.94
ATOM ATOM	935	N	ASP A		19.005	36.885	19.000	1.00 31.57
ATOM	936	CA	ASP F		18.910	38.293	19.376	1.00 33.31
ATOM	937	CB	ASP A	373	19.058	38.438	20.900	1.00 33.82
ATOM	938	CG	ASP A	373	18.989	39.902	21.381	1.00 36.02 1.00 41.04
ATOM	939	OD1	ASP A	373	18.985	40.818	20.530 22.591	1.00 41.04
ATOM	940	OD2	ASP A	373	18.972	40.227	18.649	1.00 34.95
MOTA	941	C	ASP A		20.020	39.049 39.063	19.064	1.00 34.64
ATOM	942	0	ASP A	A 373	21.198 19.636	39.678	17.553	1.00 36.75
MOTA	943	N	SER A	A 3/4	20.585	40.409	16.717	1.00 39.28
MOTA	944	CA	SER A	A 374	19.866	40.916	15.474	1.00 39.26
ATOM	945	CB	SER A	A 374 A 371	20.836	41.201	14.487	1.00 43.88
MOTA	946 947	OG C	SER A	A 374	21.325	41.581	17.378	1.00 39.94
MOTA MOTA	948	Ö	SER A	A 374	22.515	41.766	17.173	1.00 40.56
ATOM	949	й		A 375	20.626	42.366	18.186	1.00 41.01
ATOM	950	CA		A 375	21.239	43.516	18.810	1.00 41.65
ATOM	951	CB	GLN 2	A 375	20.197	44.362	19.565	1.00 42.91
ATOM	952	CG		A 375	18.913	44.675	18.767	1.00 47.27 1.00 53.49
ATOM	953	CD	GLN .	A 375	18.116	45.864	19.353	1.00 53.49
MOTA	954		GLN :	A 375	18.626	46.997 45.608	19.399 19.788	1.00 54.72
MOTA	955	NE2		A 375	16.877 22.344	43.098	19.762	1.00 40.86
MOTA	956	C		A 375	23.365	43.773	19.858	1.00 41.50
ATOM	957	O		A 375 A 376	22.155	41.987	20.463	1.00 39.20
MOTA	958 959	N CA	ASIV	A 376	23.137	41.552	21.441	1.00 38.16
ATOM ATOM	960	CB	ASN	A 376	22.438	41.264	22.766	1.00 38.40
ATOM	961	CG		A 376	21.791	42.527	23.387	1.00 40.33
MOTA	962	OD1		A 376	22.488	43.368	23.935	1.00 41.58
ATOM	963	ND2	ASN	A 376	20.452	42.644	23.301	1.00 40.49
ATOM	964	С		A 376	24.019	40.360	21.002	1.00 36.51 1.00 37.34
MOTA	965	0	ASN	A 376	24.852	39.906	21.769 19.789	1.00 37.34
ATOM	966	N		A 377	23.840 24.632	39.859 38.727	19.284	1.00 33.32
MOTA	967	CA	ASN	A 377	26.094	39.138	19.079	1.00 31.52
MOTA	968	CB	ASN	A 377 A 377	26.772	38.334	17.993	1.00 31.73
ATOM	969	CG	L ASN	A 377	26.142	37.995	16.998	1.00 33.03
MOTA	970 971	נעט	2 ASN	A 377	28.050	38.007	18.176	1.00 27.90
ATOM ATOM	972	C	ASN	A 377	24.550	37.477	20.194	1.00 31.00
ATOM	973	ŏ	ASN	A 377	25.560	37.005	20.708	1.00 31.17
ATOM	974	N	THR	A 378	23.336	36.976	20.410	1.00 29.28
ATOM	975	CA	THR	A 378	23.110	35.831	21.282	1.00 28.19
ATOM	976	CB	THR	A 378	22.643	36.241	22.727	1.00 29.06 1.00 27.46
ATOM	977			A 378	21.395	36.949	22.674 23.462	1.00 27.40
MOTA	978		2 THR	A 378	23.663	37.127 34.895	20.708	1.00 26.71
MOTA	979		THR	A 378	22.070 21.139	35.318	20.708	1.00 26.15
ATOM	980		THR	A 378 A 379	22.231	33.615	21.032	1.00 26.22
ATOM	981		VAL	A 379	21.361	32.557	20.517	1.00 24.86
MOTA	982 983		TAXT.	A 379	22.149	31.671	19.525	1.00 24.33
MOTA	983 984	CE	TVAT.	A 379	23.217	30.881	20.210	1.00 24.14
ATOM ATOM	985		2 VAL	A 379	21.210	30.747	18.777	1.00 24.47
ATOM	986		VAL	A 379	20.815		21.637	1.00 24.23
ATOM	987		VAL	A 379	21.507		22.559	1.00 24.32
MOTA	988	N	TYR	A 380	19.569	31.283	21.519	1.00 24.94

					_		20 450	22.506	1.00 25.03
ATOM	989	CA	TYR A	380	1	.8.905	30.450		1.00 24.86
ATOM	990	CB	TYR A	380		7.410	30.313	22.141	1.00 24.00
ATOM	991	CG	TYR A			6.514	29.758	23.215	
MOTA	992	CD1	TYR A	380	1	.6.614	30.197	24.535	1.00 32.61
ATOM	993	CE1	TYR A		1	5.799	29.705	25.521	1.00 32.61
	994	CZ	TYR A			L4.852	28.746	25.210	1.00 35.82
ATOM		OH	TYR A			4.038	28.236	26.193	1.00 38.69
MOTA	995	CE2	TYR A		_	4.742	28.277	23.938	1.00 34.16
ATOM	996		TYR A			15.589	28.791	22.939	1.00 32.66
MOTA	997	CD2				19.589	29.086	22.523	1.00 25.13
MOTA	998	C	TYR A			L9.563	28.416	21.514	1.00 25.44
ATOM	999	0	TYR A				28.698	23.675	1.00 25.96
ATOM	1000	N	PHE A	381		20.127		23.824	1.00 25.59
MOTA	1001	CA	PHE A			20.902	27.470		1:00 25.60
ATOM	1002	CB	PHE A			22.328	27.773	23.471	1.00 25.28
ATOM	1003	CG	PHE A			23.263	26.709	23.828	1.00 25.28
ATOM	1004	CD1	PHE A	381		23.306	25.561	23.106	1.00 20.00
ATOM	1005	CE1	PHE A	381		24.190	24.559	23.454	1.00 29.89
ATOM	1006	CZ	PHE A	381		25.049	24.733	24.537	1.00 28.60
ATOM	1007	CE2	PHE A			25.007	25.865	25.234	1.00 28.13
	1008	CD2	PHE A	381	:	24.107	26.851	24.895	1.00 27.85
MOTA	1009	C	PHE A	381		20.879	26.914	25.251	1.00 26.62
ATOM			PHE A	381		21.215	27.604	26.209	1.00 26.25
MOTA	1010	0	ASP A			20.481	25.664	25.416	1.00 27.37
MOTA	1011	N	ASP A	304		20.441	25.075	26.766	1.00 28.62
MOTA	1012	CA	ASP A	302		21.885	24.760	27.242	1.00 28.80
MOTA	1013	CB	ASP A				23.653	28.283	1.00 31.74
MOTA	1014	CG	ASP A			21.936		28.374	1.00 34.71
ATOM	1015	OD1	ASP A	382		20.973	22.859	29.045	1.00 34.71
ATOM	1016	OD2	ASP A	382		22.911	23.477		1.00 34.30
ATOM	1017	С	ASP A	382		19.705	25.888	27.853	1.00 29.36
MOTA	1018	0	ASP A	382		20.150	25.923	28.997	
MOTA	1019	N	GLY A	383		18.564	26.485	27.514	1.00 28.44
ATOM	1020	CA	GLY A			17.770	27.238	28.488	1.00 28.32
MOTA	1021	C	GLY A			17.958	28.758	28.594	1.00 27.86
	1022	ŏ	GLY A	383		17.144	29.476	29.196	1.00 29.11
MOTA	1022	N	LYS A	384		19.032	29.289	28.033	1.00 26.62
ATOM		CA	LYS A			19.241	30.731	28.108	1.00 26.42
MOTA	1024		LYS A			20.185	31.068	29.267	1.00 26.08
MOTA	1025	CB	LYS A	384		19.627	30.747	30.653	1.00 28.51
ATOM	1026	CG	LYS A	204		20.486	31.424	31.751	1.00 29.39
ATOM	1027	CD	LYS A	204		20.028	31.086	33.196	1.00 30.70
MOTA	1028	CE				20.910	31.746	34.288	1.00 29.22
MOTA	1029	NZ	LYS A			19.797	31.259	26.791	1.00 25.94
ATOM	1030	C	LYS A			20.097	30.466	25.900	1.00 26.76
MOTA	1031	О	LYS A	384		19.974	32.578	26.672	1.00 24.63
ATOM	1032	N	TYR A	. 385			33.145	25.466	1.00 24.57
ATOM	1033	CA	TYR A			20.572		25.115	1.00 24.03
MOTA	1034	CB	TYR A	. 385		19.948	34.488	24.311	1.00 24.39
ATOM	1035	CG	TYR A	. 385		18.685	34.353		
ATOM	1036	CD1	L TYR A	385		17.468	34.095		1.00 26.32
ATOM	1037	CE	L TYR A	385		16.320	34.000	24.163	1.00 20.31
ATOM	1038	CZ	TYR A	385		16.411	34.121	22.799	1.00 28.74
ATOM	1039	OH	TYR A	385		15.321	33.976	21.988	1.00 27.24
ATOM	1040	CE		385		17.628	34.353	22.195	1.00 26.89
MOTA	1041	CD2				18.723	34.458	22.944	1.00 24.65
ATOM	1042	C	TYR A	385		22.101	33.213	25.671	1.00 24.69
	1043	ŏ	TYR A	385		22.590	33.626	26.720	1.00 25.62
MOTA		N	ALA A	386		22.825	32.741	24.671	1.00 24.40
MOTA	1044		ALA A	386		24.254	32.515	24.738	1.00 24.38
ATOM	1045	CA	ALA A			24.514	31.107	24.385	1.00 23.79
ATOM	1046	CB				25.008	33.368	23.745	1.00 25.29
MOTA	1047	C	ALA A	206		24.623	33.438	22.579	1.00 26.61
MOTA	1048	0	ALA A	200		26.085	33.976	24.209	1.00 25.98
MOTA	1049	N	SER A	307		27.031	34.711	23.369	1.00 26.98
MOTA	1050	CA	SER A				35.628	24.236	1.00 26.78
ATOM	1051	CB	SER A			27.840		25.267	1.00 30.72
MOTA	1052	OG	SER A	A 387		28.416			1.00 27.67
MOTA	1053	C	SER A	387		27.985		22.787	1.00 26.96
MOTA	1054	0	SER A	A 387		27.984	32.548	23.233	1.00 20.70

ATOM	1055	N	PRO A	388	28.776	34.084	21.785	1.00 28.55
ATOM	1056	CA	PRO A	388	29.788	33.193	21.216	1.00 29.40 1.00 29.67
MOTA	1057	CB	PRO A		30.510	34.088	20.180 19.839	1.00 29.41
MOTA	1058	CG	PRO A		29.538	35.118	21.107	1.00 29.03
MOTA	1059	CD	PRO A	388	28.781	35.393 32.659	22.250	1.00 30.29
MOTA	1060	С	PRO A	388	30.775	31.581	22.052	1.00 30.55
MOTA	1061	0	PRO A	388	31.346 30.972	33.389	23.338	1.00 31.61
MOTA	1062	N	ASP A		31.864	32.951	24.406	1.00 32.74
MOTA	1063	CA	ASP A	303	31.882	33.986	25.510	1.00 34.07
ATOM	1064	CB CG	ASP A	389	32.640	35.207	25.127	1.00 39.93
MOTA	1065 1066	OD1	ASP A	389	33.325	35.175	24.070	1.00 47.04
ATOM ATOM	1067	OD2	ASP A	389	32.601	36.259	25.813	1.00 46.60
ATOM	1068	C	ASP A		31.484	31.614	25.044	1.00 31.53
ATOM	1069	Õ	ASP A	389	32.359	30.893	25.528	1.00 31.63 1.00 29.87
ATOM	1070	N	VAL A	390	30.189	31.317	25.069	1.00 29.20
ATOM	1071	CA	VAL A	390	29.667	30.079 30.083	25.616 25.572	1.00 29.33
MOTA	1072	CB	VAL A	390	28.119	28.705	25.643	1.00 29.50
MOTA	1073	_	VAL A	390	27.579 27.582	30.907	26.704	1.00 29.08
MOTA	1074	CG2	VAL A VAL A		30.183	28.865	24.870	1.00 28.35
MOTA	1075	C	VAL A		30.307	27.811	25.440	1.00 28.58
MOTA	1076 1077	N O	PHE A	391	30.551	29.038	23.610	1.00 28.30
MOTA MOTA	1077	CA	PHE A	391	31.038	27.943	22.785	1.00 27.98
ATOM	1079	CB	PHE A	391	30.365	28.034	21.431	1.00 27.73
MOTA	1080	CG	PHE A	391	28.882	28.039	21.514	1.00 26.60 1.00 25.13
ATOM	1081	CD1		391	28.180	29.233	21.549	1.00 25.13
MOTA	1082	CE1	PHE A	391	26.814	29.228	21.640 21.674	1.00 24.94
MOTA	1083	CZ	PHE A		26.129	28.025 26.837	21.650	1.00 24.26
MOTA	1084	CE2	PHE A		26.812 28.180	26.840	21.574	1.00 25.61
ATOM	1085	CD2	PHE A	391	32.566	27.838	22.571	1.00 28.31
MOTA	1086	C	PHE A	391	33.018	27.054	21.729	1.00 27.05
MOTA	1087 1088	N O	LYS A	392	33.328	28.579	23.356	1.00 29.26
ATOM ATŌM	1089	CA	LYS A	392	34.795	28.578	23.281	1.00 31.34
ATOM	1090	CB	LYS A	392	35.366	29.495	24.377	1.00 32.61
ATOM	1091	CG	LYS A	392	36.861	29.771	24.281	1.00 35.79 1.00 39.49
ATOM	1092	CD	LYS A	392	37.301	30.620	25.474 25.699	1.00 39.49 1.00 41.94
MOTA	1093	CE	LYS A	392	38.826	30.579 31.071	27.075	1.00 42.28
MOTA	1094	NZ	LYS A	392	39.185 35.456	27.202	23.366	1.00 31.54
MOTA	1095	C	LYS A	392	36.322	26.898	22.567	1.00 31.50
ATOM	1096	O N	SER A	3 3 3 2 2	35.008	26.343	24.288	1.00 32.67
MOTA	1097 1098	CA	SER A	393	35.571	25.003	24.431	1.00 32.44
ATOM ATOM	1099	CB	SER A	393	34.989	24.270	25.624	1.00 32.78
ATOM	1100	OG	SER A	¥ 393	35.056	25.069	26.784	1.00 35.03
ATOM	1101	C	SER A	A 393		24.110	23.240	1.00 32.29 1.00 32.31
ATOM	1102	0	SER A	A 393	36.048	23.062	23.169 22.303	1.00 32.31
MOTA	1103	N	LEU A	A 394	34.534 34.436	24.465 23.653	21.121	1.00 31.95
ATOM	1104	CA	LEU A	A 394	33.304	24.091	20.195	1.00 32.22
ATOM	1105	CB	LEU A	A 394 A 394	31.829	23.898	20.560	1.00 30.03
ATOM	1106	CG	LEU A	n 394	30.964	24.445	19.463	1.00 27.50
MOTA	1107 1108	CD.	LEU Z	A 394	31.547	22.458	20.809	1.00 31.13
ATOM ATOM	1109	C	LEU Z	A 394	35.720	23.720	20.316	1.00 32.56
ATOM	1110	ŏ	LEU	A 394	35.948		19.493	1.00 32.76
ATOM	1111	N	GLY 2	A 395	36.520		20.498	1.00 35.25
ATOM	1112	CA	GLY :	A 395	37.717			1.00 36.37 1.00 37.83
ATOM	1113	С	GLY .	A 395	37.426			1.00 37.83
MOTA	1114		GLY .	A 395	38.249 36.300			1.00 38.87
MOTA	1115			A 396	35.877			
ATOM	1116		CYS	A 396 A 396	34.603			1.00 40.04
MOTA	1117		CID	A 396	34.493			1.00 47.12
ATOM ATOM	1118 1119		CYS	A 396	35.483		16.522	1.00 38.76
ATOM	1120		CYS	A 396	34.364		16.063	1.00 37.44
MION		•						

		97 36.359	28.747	16.928	1.00 38.45
MOTA	1121 N GLU A 39		30.158	16.905	1.00 39.15
MOTA	1122 CA GLU A 3		31.064	17.392	1.00 39.98
MOTA	1123 CB GLU A 39		30.611	18.702	1.00 45.20
ATOM		-	31.254	19.991	1.00 51.31
MOTA			31.041	20.323	1.00 55.26
ATOM			31.920	20.717	1.00 53.17
MOTA	1127 OE2 GLU A 3		30.605	15.520	1.00 37.80
MOTA	1128 C GLU A 3 1129 O GLU A 3		31.296	15.465	1.00 37.56
MOTA			30.197	14.423	1.00 37.26
MOTA			30.640	13.091	1.00 37.80
MOTA			30.253	12.000	1.00 39.29
ATOM			31.019	12.097	1.00 42.86
ATOM			32.024	12.844	1.00 48.94
MOTA			30.660	11.450	1.00 47.39
ATOM	1135 OD2 ASP A 3 1136 C ASP A 3		30.103	12.676	1.00 35.53
MOTA	1137 O ASP A 3		30.848	12.182	1.00 35.67
ATOM	1138 N PHE A 3		28.814	12.852	1.00 33.02
ATOM	1139 CA PHE A 3		28.264	12.574	1.00 31.62
MOTA	1140 CB PHE A 3		26.754	12.735	1.00 31.05
ATOM ATOM	1141 CG PHE A 3		26.151	12.729	1.00 30.78
ATOM	1142 CD1 PHE A 3		26.027	11.567	1.00 30.86
ATOM	1143 CE1 PHE A 3	99 29.437	25.502	11.561	1.00 31.41
ATOM	1144 CZ PHE A 3	199 28.856	25.092	12.742	1.00 31.17
MOTA	1145 CE2 PHE A 3	399 29.526	25.243	13.905	1.00 30.20
ATOM	1146 CD2 PHE A 3	39.797	25.777	13.906	1.00 29.57
MOTA	1147 C PHE A 3	39 31.665	28.932	13.466	1.00 30.38
ATOM	1148 O PHE A 3	39 30.567	29.240	13.014	1.00 30.06 1.00 29.09
ATOM	1149 N ILE A	100 31.975	29.187	14.718	1.00 29.09
ATOM	1150 CA ILE A	100 30.988	29.793	15.584	1.00 28.21
ATOM	1151 CB ILE A		29.709	17.022	1.00 27.45
ATOM	1152 CG1 ILE A		28.255	17.501 17.525	1.00 27.35
ATOM	1153 CD1 ILE A	30.013	27.629	17.525	1.00 27.33
MOTA	1154 CG2 ILE A	400 30.557	30.501 31.213	15.132	1.00 28.30
ATOM	1155 C ILE A	400 30.717	31.652	15.105	1.00 27.29
MOTA	1156 O ILE A		31.949	14.758	1.00 27.64
MOTA	1157 N SER A		33.329	14.298	1.00 28.85
MOTA	1158 CA SER A 4		34.152	14.224	1.00 28.93
ATOM			33.761	13.129	1.00 35.10
ATOM			33.397	12.997	1.00 27.77
MOTA	1161 C SER A 6 1162 O SER A		34.283	12.818	1.00 28.99
MOTA	1162 O SER A		32.423	12.133	1.00 27.14
MOTA	1164 CA PHE A		32.276	10.923	1.00 27.41
MOTA MOTA	1165 CB PHE A	402 30.800	31.145	10.137	1.00 27.67
ATOM	1166 CG PHE A	402 30.303	30.940	8.733	1.00 30.03
ATOM	1167 CD1 PHE A	402 29.486	31.840	8.091	1.00 31.94
MOTA	1168 CE1 PHE A	402 29.061	31.618	6.813	1.00 30.13
ATOM	1169 CZ PHE A	402 29.438	30.512	6.124	1.00 30.57 1.00 33.09
ATOM	1170 CE2 PHE A	402 30.266	29.595	6.712	1.00 33.09
ATOM	1171 CD2 PHE A	402 30.704	29.815	8.030	1.00 34.00
ATOM	1172 C PHE A	402 28.657	31.992	11.290 10.717	1.00 25.94
ATOM	1173 O PHE A	402 27.733	32.571	12.280	1.00 26.02
MOTA	1174 N VAL A	403 28.416		12.669	1.00 25.17
MOTA	1175 CA VAL A	403 27.035 403 26.967		13.797	1.00 24.18
MOTA	1176 CB VAL A			14.394	1.00 25.35
MOTA	1177 CG1 VAL A		_	13.255	1.00 24.23
MOTA	1178 CG2 VAL A			13.158	1.00 24.80
ATOM	1179 C VAL A 1180 O VAL A			12.831	1.00 24.70
ATOM					1.00 24.99
MOTA					1.00 25.96
MOTA	1182 CA PHE A 1183 CB PHE A			15.719	1.00 26.02
ATOM ATOM	1184 CG PHE A		33.880	17.037	
ATOM			32.614		1.00 26.60
ATOM		404 27.087	31.962	18.535	1.00 27.71
AION					

							40 475	1.00 26.31
ATOM	1187	CZ	PHE A	404	26.358	32.572	19.475	
ATOM	1188	CE2	PHE A	404	25.881	33.846	19.230	1.00 29.49
ATOM	1189	CD2	PHE A	404	26.178	34.501	18.010	1.00 28.52
ATOM	1190	Č	PHE A		26.232	35.121	13.488	1.00 26.66
	1191	ŏ	PHE A		25.278	35.891	13.515	1.00 27.41
MOTA			GLU A	105	27.151	35.166	12.537	1.00 27.79
MOTA	1192	N			27.078	36.165	11.487	1.00 27.80
MOTA	1193	CA	GLU A	405		36.163	10.623	1.00 28.35
ATOM	1194	CB	GLU A	405	28.339		9.384	1.00 31.23
MOTA	1195	CG	GLU A	405	28.147	37.016	8.769	1.00 35.82
ATOM	1196	CD	GLU A		29.446	37.528		
ATOM	1197	OE1	GLU A	405	30.552	37.009	9.096	
ATOM	1198	OE2	GLU A		29.334	38.448	7.937	1.00 35.95
ATOM	1199	C	GLU A	405	25.861	35.864	10.629	1.00 27.96
	1200	ŏ	GLU A		25.126	36.773	10.228	1.00 25.82
ATOM			PHE A		25.658	34.576	10.373	1.00 27.97
MOTA	1201	N	PHE A		24.508	34.148	9.629	1.00 29.23
MOTA	1202	CA			24.549	32.656	9.326	1.00 28.50
ATOM	1203	CB	PHE A			32.229	8.434	1.00 29.33
MOTA .	1204	CG	PHE A		23.459		7.058	1.00 31.26
ATOM	1205	CD1	PHE A	406	23.588	32.396		1.00 29.99
ATOM	1206	CE1	PHE A		22.574	32.049	6.214	
ATOM	1207	CZ	PHE A		21.389	31.531	6.737	
MOTA	1208	CE2	PHE A	406	21.253	31.340	8.104	1.00 30.00
ATOM	1209	CD2		406	22.277	31.698	8.949	1.00 27.04
	1210	C	PHE A	406	23.204	34.511	10.367	1.00 30.08
ATOM	1211	ŏ	PHE A	406	22.238	34.936	9.746	1.00 29.57
MOTA			GLY A		23.186	34.337	11.681	1.00 31.28
MOTA	1212	N	GLY A		22.009	34.643	12.485	1.00 31.96
ATOM	1213	CA			21.699	36.116	12.401	1.00 33.32
MOTA	1214	C	GLY A			36.539	12.135	1.00 32.80
MOTA	1215	0	GLY A	407	20.581	36.915	12.577	1.00 35.20
MOTA	1216	N	LYS A	408	22.729		12.430	1.00 36.71
ATOM	1217	ca	LYS A	. 408	22.586	38.344		
ATOM	1218	CB	LYS A	. 408	23.931	38.993	12.688	
ATOM	1219	CG	LYS A	. 408	23.845	40.473	12.958	
ATOM	1220	CD	LYS A	408	25.125	41.000	13.605	1.00 44.55
ATOM	1221	CE	LYS A		25.143	40.758	15.121	1.00 46.16
	1222	NZ	LYS A		26.310	41.466	15.786	1.00 47.26
MOTA	1223	C	LYS A		22.090	38.756	11.033	1.00 37.33
MOTA			LYS A		21.233	39.637	10.881	1.00 37.08
ATOM	1224	0	SER A		22.610	38.106	10.005	1.00 37.62
ATOM	1225	N			22.258	38.499	8.649	1.00 38.03
MOTA	1226	CA	SER A		23.258	37.906	7.681	1.00 37.87
MOTA	1227	CB	SER A		22.671	37.759	6.421	1.00 43.04
MOTA	1228	OG	SER A			38.139	8.273	1.00 37.59
ATOM	1229	C	SER A	409	20.816	38.891	7.596	1.00 37.65
MOTA	1230	0	SER P	409	20.146			1.00 38.00
ATOM	1231	N	LEU A	410	20.330	36.994	8.730	
MOTA	1232	CA	LEU F		18.944	36.599	8.476	
ATOM	1233	CB	LEU F	410	18.771	35.108	8.728	1.00 37.93
ATOM	1234	CG	LEU A		17.711	34.363	7.930	1.00 39.48
MOTA	1235	CD1	L LEU A		17.866	34.566	6.431	1.00 40.64
MOTA	1236	CD	LEU A	410	17.795	32.873	8.280	1.00 39.84
	1237	C	LEU A		17.969	37.447	9.323	1.00 37.89
ATOM			LEU 2		16.907	37.826	8.859	1.00 36.02
ATOM	1238	0	DEO A	1 410	18.344	37.745	10.558	1.00 39.15
MOTA	1239	N	CYS I	3 411 8 111	17.552	38.634	11.416	1.00 40.62
MOTA	1240	CA	CYS	A 411	18.243	38.819	12.753	1.00 41.09
MOTA	1241	СВ		A 411		37.449	13.893	1.00 41.89
MOTA	1242	SG	CYS	A 411	18.069		10.822	1.00 41.43
MOTA	1243	С	CYS I	A 411	17.371	40.029		1.00 41.43
MOTA	1244	0	CYS 7	A 411	16.301	40.596	10.880	1.00 42.39
ATOM	1245	N	SER I	A 412	18.433	40.579	10.253	1.00 42.33
ATOM	1246		SER A	A 412	18.381	41.897	9.641	1.00 43.17
ATOM	1247	CB	SER 2	A 412	19.756	42.278	9.067	1.00 42.83
ATOM	1248		SER	A 412	19.897	41.811	7.730	1.00 43.89
ATOM	1249		SER	A 412	17.325		8.534	
	1250			A 412	17.030		8.072	1.00 45.40
ATOM	1250		MET	A 413	16.771		8.085	1.00 43.86
MOTA	1251		MET	A 413	15.732		7.065	
ATOM	1636	CA						

ATOM ATOM ATOM ATOM ATOM ATOM ATOM ATOM	1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267	CB MET A 413 CG MET A 413 SD MET A 413 CE MET A 413 C MET A 413 O MET A 413 N HIS A 414 CA HIS A 414 CB HIS A 414 CG HIS A 414 ND1 HIS A 414 ND1 HIS A 414 NE2 HIS A 414 CCD HIS A 414 CD2 HIS A 414 CD2 HIS A 414 C HIS A 414	15.874 17.179 17.293 19.021 14.319 13.354 14.207 12.917 12.369 13.414 13.905 14.830 14.956 14.078 11.920 10.905	39.740 39.724 38.227 38.123 40.920 41.154 40.686 40.694 42.124 43.131 43.252 44.198 44.694 44.694 44.046 39.867 40.380	6.102 5.375 4.484 4.084 7.666 6.948 8.969 9.651 9.831 10.202 11.484 11.511 10.290 9.452 8.867 8.397	1.00 44.68 1.00 45.77 1.00 52.29 1.00 52.15 1.00 44.82 1.00 45.27 1.00 44.42 1.00 45.37 1.00 46.54 1.00 49.03 1.00 52.74 1.00 53.78 1.00 53.78 1.00 51.02 1.00 44.54 1.00 45.13
MOTA MOTA	1268 1269	N LEU A 415	12.221	38.586	8.712	1.00 43.37
MOTA	1270	CA LEU A 415	11.345	37.696	7.992 7.563	1.00 42.05 1.00 42.25
ATOM	1271	CB LEU A 415	12.098 13.274	36.448 36.739	6.635	1.00 42.37
MOTA	1272	CG LEU A 415 CD1 LEU A 415	14.213	35.584	6.615	1.00 43.50
MOTA MOTA	1273 1274	CD2 LEU A 415	12.736	37.013	5.254	1.00 42.77
ATOM	1275	C LEU A 415	10.200	37.311	8.889	1.00 41.21 1.00 40.43
ATOM	1276	O LEU A 415	10.379	37.116 37.191	10.073 8.310	1.00 40.43
ATOM	1277	N THR A 416 CA THR A 416	9.019 7.852	36.771	9.050	1.00 39.80
ATOM	1278 1279	CA THR A 416 CB THR A 416	6.587	37.152	8.269	1.00 39.84
MOTA MOTA	1280	OG1 THR A 416	6.623	36.538	6.978	1.00 39.74
ATOM	1281	CG2 THR A 416	6.546	38.636	7.950 9.203	1.00 39.98 1.00 39.01
ATOM	1282	C THR A 416	7.890 8.698	35.270 34.609	8.553	1.00 38.71
MOTA	1283	O THR A 416 N GLU A 417	7.004	34.728	10.035	1.00 38.46
MOTA MOTA	1284 1285	CA GLU A 417	6.925	33.289	10.241	1.00 38.70
MOTA	1286	CB GLU A 417	5.879	32.940	11.318	1.00 38.85 1.00 41.11
ATOM	1287	CG GLU A 417	6.350 7.583	33.068 32.225	$\frac{1}{2}.768$ 13.115	1.00 41.56
MOTA	1288	CD GLU A 417 OE1 GLU A 417	7.436	31.070	13.527	1.00 40.66
ATOM ATOM	1289 1290	OE2 GLU A 417	8.707	32.744	13.014	1.00 44.69
ATOM	1291	C GLU A 417	6.599	32.558	8.921	1.00 38.40 1.00 37.21
ATOM	1292	O GLU A 417	7.140 5.717	31.493 33.122	8.629 8.117	1.00 37.21
MOTA	1293	N ASP A 418 CA ASP A 418	5.382	32.489	6.845	1.00 39.36
MOTA MOTA	1294 1295	CA ASP A 418 CB ASP A 418	4.134	33.115	6.221	1.00 40.08
ATOM	1296	CG ASP A 418	2.858	32.783	7.007	1.00 44.36 1.00 50.10
ATOM	1297	OD1 ASP A 418	2.931	31.961 33.282	7.953 6.742	1.00 48.86
MOTA	1298	OD2 ASP A 418 C ASP A 418	1.736 6.540	32.531	5.865	1.00 38.10
MOTA	1299 1300		6.712	31.634	5.057	1.00 37.14
MOTA MOTA	1301	N GLUA 419	7.311	33.602	5.925	1.00 37.67 1.00 37.99
ATOM	1302	CA GLU A 419	8.479	33.730	5.074 5.163	1.00 37.99
MOTA	1303		9.062 8.269	35.165 36.175	4.336	1.00 40.90
ATOM	1304		8.530	37.629	4.682	1.00 41.76
MOTA MOTA	1305 1306	440	9.193	37.895	5.685	1.00 43.26
MOTA	1307	OE2 GLU A 419	8.059	38.512	3.938	1.00 45.04 1.00 36.84
MOTA	1308	C GLU A 419	9.519 10.106		5.459 4.590	1.00 36.16
MOTA	1309		9.708		6.760	1.00 35.93
MOTA MOTA	1310 1311		10.695	31.488	7.233	1.00 35.74
MOTA		CB ILE A 420	10.899		8.740	1.00 36.17 1.00 38.07
MOTA	1313	CG1 ILE A 420	11.712 11.838		9.008 10.464	
ATOM			11.838			1.00 36.15
MOTA MOTA			10.311	30.085	6.856	
ATOM		O ILE A 420	11.156	29.282		
ATOM			9.013	29.813	6.914	1.00 33.91

ATOM ATOM ATOM ATOM ATOM ATOM	1319 1320 1321 1322 1323 1324	CB C O N	ALA A ALA A ALA A ALA A LEU A LEU A	421 421 421 422	8.459 7.024 8.676 9.065 8.384 8.508	28.535 28.543 28.194 27.064 29.140 28.871	6.813 5.084 4.769 4.188 2.773	1.00 32.70 1.00 33.68 1.00 32.56 1.00 31.53 1.00 31.71 1.00 32.27 1.00 33.13
ATOM	1325	CB	LEU A	422	7.779	29.923 29.927	1.948 2.141	1.00 33.13
MOTA	1326	CG	LEU A	422	6.261 5.611	30.995	1.361	1.00 40.39
MOTA	1327	CDI	LEU A LEU A	422	5.677	28.631	1.696	1.00 40.84
ATOM ATOM	1328 1329	CD2	LEU A	422	9.972	28.770	2.367	1.00 31.63
ATOM	1330	ŏ	LEU A	422	10.319	28.037	1.452	1.00 31.16 1.00 31.46
ATOM	1331	N	PHE A	423	10.828	29.525 29.487	3.046 2.758	1.00 31.40
MOTA	1332	CA	PHE A	423	12.247 12.957	30.654	3.414	1.00 32.18
MOTA	1333	CB CG	PHE A	423 423	14.396	30.795	3.015	1.00 32.59
ATOM	1334 1335	CD1	PHE A	423	14.800	30.673	1.696	1.00 34.16
MOTA MOTA	1336	CE1	PHE A	423	16.128	30.853	1.357	1.00 34.47 1.00 33.24
ATOM	1337	CZ	PHE A	423	17.056	31.142 31.246	2.336 3.647	1.00 33.24
ATOM	1338	CE2	PHE A	423	16.654 15.342	31.240	3.977	1.00 33.39
ATOM	1339		PHE A	. 423 . 423	12.852		3.239	1.00 31.47
ATOM ATOM	1340 1341	C O	PHE A	423	13.743	27.612	2.592	1.00 31.65
ATOM	1342	Ŋ	SER A	424	12.379	27.678	4.387	1.00 30.47 1.00 29.56
MOTA	1343	CA	SER A	424	12.730		4.874 6.182	1.00 28.62
ATOM	1344	CB	SER A	424	12.038 12.536		7.175	1.00 30.82
MOTA	1345	OG C	SER A	424	12.337		3.897	1.00 28.62
MOTA MOTA	1346 1347	Ö	SER A	424	13.121	24.391	3.610	1.00 28.23
ATOM	1348	Ŋ	ALA A	425	11.106		3.433	1.00 28.24 1.00 28.61
ATOM	1349	CA	ALA A	425	10.643		2.465 2.249	1.00 28.26
ATOM	1350	CB	ALA A	425	9.139 11.389		1.123	1.00 29.02
ATOM	1351	C	ALA A	4 425	11.530		0.434	1.00 30.06
ATOM ATOM	1352 1353	N	PHE A	426	11.873	25.567	0.778	1.00 30.03
ATOM	1354	CA	PHE A	426	12.61		-0.451 -0.637	1.00 31.03 1.00 30.64
ATOM	1355	CB	PHE Z	A 426	12.751 13.479		-1.875	1.00 33.04
MOTA	1356	CG	PHE A	A 426	12.835		-3.094	1.00 32.88
MOTA	1357 1358		PHE	A 426	13.524		-4.238	1.00 34.86
MOTA MOTA	1359		PHE	A 426	14.872	2 28.293	-4.189	1.00 34.01 1.00 34.91
MOTA	1360	CE2	PHE	A 426	15.51		-2.986 -1.834	1.00 35.40
ATOM	1361		PHE	A 426	14.81° 14.00		-0.447	1.00 31.56
ATOM	1362		PHE	A 426 A 426	14.32		-1.329	1.00 31.28
ATOM ATOM	1363 1364			A 427	14.84	6 25.426	0.557	1.00 32.26
MOTA	1365		VAL .	A 427	16.20	4 24.824	0.597 1.524	1.00 33.10 1.00 33.53
MOTA	1366	CB	VAL	A 427	17.16 17.20	8 25.602 5 27.072	1.140	1.00 34.66
MOTA	1367		1 VAL 2 VAL	A 427	16.77		2.953	1.00 35.57
MOTA	1368 1369		VAL.	A 427	16.18		0.987	1.00 32.54
MOTA MOTA	1370		VAL	A 427	17.18	2 22.637	0.881	1.00 32.60 1.00 33.17
MOTA	1371		LEU	A 428	15.03		1.433 1.788	
ATOM	1372			A 428	14.89 13.75		2.751	
ATOM	1373		LEU	A 428 A 428	13.73		3.346	1.00 35.63
MOTA MOTA	1374 1375		1 LEU	A 428	14.75	1 19.913	4.473	
ATOM	137		2 LEU	A 428	12.34		3.830	
MOTA	137	7 C	LEU	A 428	14.64		0.563 0.444	
MOTA	137		LEU	A 428 A 429	15.18 13.76		-0.315	1.00 33.59
MOTA	1379 1389		MET	A 429	13.44		-1.521	1.00 34.98
MOTA MOTA			MET	A 429	11.97	7 20.670	-1.871	
ATOM			MET	A 429	11.03		-0.714 -0.205	
MOTA	138			A 429	10.84 10.46			
MOTA	138	4 CE	MET	A 429	10.40			
			•					

	1205	_	MET A	129	14.293	20.979	-2.639	1.00 35.57
ATOM	1385	C	MET A		13.772	21.578	-3.556	1.00 35.78
ATOM	1386	0	SER A	423 423	15.602	20.813	-2.559	1.00 36.04
ATOM	1387	N	SER A	430	16.465	21.298	-3.608	1.00 37.23
ATOM	1388	CA	SER A	430 430	17.782	21.792	-3.060	1.00 37.79
MOTA	1389	CB	SER A	430 430	17.672	22.092	-1.698	1.00 40.76
ATOM	1390	og	SER A	430	16.760	20.144	-4.507	1.00 37.02
MOTA	1391	C	SER A	430	17.088	19.054	-4.034	1.00 37.47
MOTA	1392	0	SER A	430	16.683	20.375	-5.800	1.00 37.33
MOTA	1393	N	ALA A	431		19.301	-6.749	1.00 38.02
ATOM	1394	CA	ALA A	431	16.869	19.581	-7.999	1.00 38.37
MOTA	1395	CB	ALA A	431	16.086	19.088	-7.071	1.00 39.47
MOTA	1396	С	ALA A	431	18.332	18.155	-7.801	1.00 40.70
MOTA	1397	0	ALA A	431	18.675		-6.528	1.00 40.30
MOTA	1398	N	ASP A	432	19.219	19.916	-6.853	1.00 41.30
MOTA	1399	CA	ASP A		20.619	19.731	-7.201	1.00 42.25
ATOM	1400	CB	ASP A	432	21.304	21.041	-6.217	1.00 45.95
ATOM	1401	CG	ASP A	432	21.026	22.093	-6.001	1.00 48.76
MOTA	1402	OD1	ASP A	432	21.919	22.947	-5.610	1.00 53.78
MOTA	1403	OD2	ASP A	432	19.930	22.144	-5.818	1.00 40.17
MOTA	1404	С	ASP A	432	21.425	18.985		1.00 42.18
MOTA	1405	0	ASP A	432	22.623	18.843	-5.968	1.00 38.39
ATOM	1406	N	ARG A	433	20.810	18.440	-4.800	1.00 37.16
ATOM	1407	CA	ARG A		21.597	17.625	-3.915	1.00 37.10
MOTA	1408	CB	ARG A		20.744	17.081	-2.804	1.00 30.78
ATOM	1409	CG	ARG A		19.976	18.117	-2.084	1.00 37.00
ATOM	1410	CD	ARG A		20.810	19.149	-1.420	
ATOM	1411	NE	ARG A	433	19.938	19.958	-0.589	1.00 38.16 1.00 37.36
ATOM	1412	CZ	ARG A	433	20.335	20.952	0.180	1.00 37.30
ATOM	1413	NH1	ARG A	433	21.611	21.301	0.238	1.00 34.55
ATOM	1414	NH2	ARG A		19.443	21.633	0.885	1.00 38.38
ATOM	1415	С	ARG A	433	22.145	16.450	-4.731	1.00 37.08
ATOM	1416	0	ARG A	433	21.441	15.925	-5.593	1.00 35.43
ATOM	1417	N	SER A	434	23.370	16.022	-4.430	1.00 36.72
MOTA	1418	CA	SER A	434	23.963	14.877	-5.105	1.00 36.76
ATOM	1419	CB	SER A	434	25.390	14.603	-4.593	1.00 36.85
ATOM	1420	OG	SER A		26.176	15.757	-4.604	1.00 38.46 1.00 36.80
ATOM	1421	C	SER A		23.196	13.630	-4.782	1.00 35.80
ATOM	1422	0	SER A	434	22.660	13.481	-3.670	
MOTA	1423	N	TRP A	435	23.206	12.720	-5.754	1.00 36.33 1.00 36.22
ATOM	1424	CA	TRP A		22.706	11.376	-5.614	1.00 36.22
ATOM	1425	CB	TRP A		23.314	10.715	-4.376	1.00 38.37
ATOM	1426	CG	TRP A		24.778	10.979	-4.204	1.00 40.89
ATOM	1427	CD1	L TRP A	435	25.379	11.502	-3.115	1.00 40.89
ATOM	1428	NE:	L TRP A	435	26.733	11.585	-3.315	1.00 41.13
MOTA	1429	CE	2 TRP A	435	27.026	11.109	-4.560	1.00 39.09
ATOM	1430	CD2	2 TRP A	435	25.825	10.717	-5.147	1.00 38.76
MOTA	1431	CE:	3 TRP A	435	25.862	10.172	-6.425	
ATOM	1432	CZ:	3 TRP A	435		10.049	-7.063	1.00 41.35
ATOM	1433	CH	2 TRP A	435	28.250	10.450	-6.451	1.00 41.33
MOTA	1434	CZ	2 TRP A	435	28.249	10.976	-5.195	1.00 36.43
MOTA	1435	C	TRP A	435	21.193	11.264	-5.575	1.00 35.43
ATOM	1436	0	TRP A	. 435	20.674	10.269	-5.110	1.00 33.92
MOTA	1437	N	LEU A	436	20.483	12.272	-6.048	
ATOM	1438	CA	LEU A	436	19.013	12.185	-6.139	1.00 38.64
ATOM	1439	CB	LEU A	436	18.419	13.585	-6.194	1.00 38.27
ATOM	1440	CG	LEU A	436	18.387	14.376	-4.902	1.00 37.94
ATOM	1441	CD	1 LEU A	436	17.844	15.752	-5.190	1.00 38.90
ATOM	1442	CD	2 LEU A	436	17.547	13.667	-3.885	1.00 37.76
ATOM	1443		LEU A	436	18.531	11.436	-7.394	1.00 40.22
ATOM	1444		LEU A	436	19.022	11.691	-8.497	1.00 40.43
ATOM	1445	N	GLN A	437	17.542	10.562	-7.241	1.00 42.27
ATOM	1446		GLN A	437	16.981	9.825	-8.370	1.00 43.95 1.00 44.38
ATOM	1447		GLN A	437	16.334	8.537	-7.896	
MOTA	1448	CG		437	17.247	7.710	-7.059	1.00 46.96
ATOM	1449	CD	GLN A	437	16.647	6.389	-6.653	1.00 50.03 1.00 54.83
MOTA	1450	OE	1 GLN A	4 437	15.546	6.043	-7.084	T.00 24.03

ATOM	1451	NE2	GLN A	437	17.370	5.640	-5.826	1.00 50.03
MOTA	1452	C	GLN A	437	15.958	10.644	-9.136	1.00 44.68 1.00 45.04
ATOM	1453	0	GLN A		16.051		-10.346	1.00 45.84
MOTA	1454	N	GLU A		15.000	11.221	-8.433 -9.093	1.00 45.04
MOTA	1455	CA	GLU A		13.933	11.977 11.716	-8.360	1.00 47.49
MOTA	1456	CB	GLU A		12.628	10.254	-8.005	1.00 49.80
ATOM	1457	CG	GLU A		12.433 11.318	10.254	-7.011	1.00 54.24
MOTA	1458	CD	GLU A GLU A	430	10.145	10.256	-7.410	1.00 55.09
ATOM	1459	OE1 OE2	GLU A	430 430	11.625	9.744	-5.832	1.00 58.98
ATOM	1460 1461	C	GLU A	438	14.169	13.475	-9.154	1.00 46.63
ATOM ATOM	1462	Ö	GLU A	438	13.399	14.242	-8.586	1.00 47.40
ATOM	1463	N	LYS A		15.192	13.897	-9.887	1.00 46.50
ATOM	1464	CA	LYS A	439	15.535	15.311	-9.995	1.00 45.87
ATOM	1465	СВ	LYS A	439	16.834		-10.794	1.00 46.05 1.00 48.48
ATOM	1466	CG	LYS A		18.096		-10.113	1.00 48.48
ATOM	1467	CD	LYS A		19.417		-10.247 -8.875	1.00 54.04
MOTA	1468	CE	LYS A	439	20.205	15.702 16.236	-8.775	1.00 53.95
ATOM	1469	NZ	LYS A		21.624 14.405	16 129	-10.609	1.00 45.17
ATOM	1470	C	LYS A		14.149	17.248	-10.179	1.00 44.73
MOTA	1471	O N	VAL A		13.723	15.582	-11.607	1.00 44.46
MOTA	1472 1473	N CA	VAL A		12.665	16.324	-12.279	1.00 43.79
ATOM ATOM	1474	CB	VAL A	440	12.234	15.633	-13.601	1.00 44.85
MOTA	1475		VAL A		10.895		-14.096	1.00 43.93
ATOM	1476	CG2	VAL A	440	13.359	15.762	-14.686	1.00 44.89
ATOM	1477	C	VAL A	440	11.437	16.574	-11.385	1.00 42.76 1.00 42.48
ATOM	1478	0	VAL A	440	10.908	17.667	-11.371	1.00 42.48
ATOM	1479	N	LYS A		10.981	15.582	-10.638 -9.737	1.00 42.10
MOTA	1480	CA	LYS A	441	9.842	14.469	-9.167	1.00 42.37
MOTA	1481	CB	LYS A	441	9.337 8.268	14.551	-8.058	1.00 44.18
MOTA	1482	CG	LYS A	1 44I	7.770	13.145	-7.635	1.00 46.69
ATOM	1483 1484	CD	LYS A	1 441	7.415	13.029	-6.135	1.00 48.06
ATOM ATOM	1485	NZ	LYS A	441	6.374	13.988	-5.640	1.00 50.40
ATOM	1486	C	LYS A	441	10.222	16.812	-8.621	1.00 41.30
MOTA	1487	ŏ	LYS A		9.493	17.751	-8.337	1.00 41.41
ATOM	1488	N	ILE A	4 442	11.384	16.639	-8.016	1.00 40.14 1.00 39.47
MOTA	1489	CA	ILE A		11.792	17.530	-6.947	1.00 39.47
ATOM	1490	CB		442	13.092	17.036 15.709	-6.347 -5.642	1.00 37.84
MOTA	1491	CG1		A 442	12.817 14.038	14.971	-5.155	1.00 36.84
MOTA	1492	CD1		A 442 A 442	13.694	18.109	-5.421	1.00 38.41
ATOM	1493	CG2 C		A 442	11.924	18.939	-7.475	1.00 40.04
MOTA MOTA	1494 1495	Ö	TLE	A 442	11.519	19.907	-6.828	1.00 39.89
ATOM	1496	N	GLU	A 443	12.474	19.068		1.00 40.56
MOTA	1497	CA		A 443	12.583	20.380	-9.305	1.00 41.62
ATOM	1498	CB	GLU 2	A 443	13.325	20.252	-10.625	1.00 42.43 1.00 46.01
ATOM	1499	CG	GLU :	A 443	13.473	21.556	-11.384	1.00 46.01
MOTA	1500	CD		A 443	14.586	22.409	-10.832 -10.224	1.00 58.50
MOTA	1501		L GLU		15.520 14.540	21.640	-10.224	1.00 56.77
MOTA	1502	OE:	Z GLU .	A 443	11.221	21.041		1.00 41.19
MOTA	1503	C	GLU .	A 443 A 443	11.051	22.217		1.00 41.75
MOTA	1504	И	T.VC	A 444	10.241		-10.027	1.00 41.34
	1505 1506	CA		A 444	8.918	20.906	-10.222	1.00 41.91
MOTA MOTA	1507	CB	LYS	A 444	7.954	19.921	-10.887	1.00 42.50
MOTA	1508	CG	LYS	A 444	8.359	19.402	-12.287	1.00 46.11
ATOM	1509	CD	LYS	A 444	8.622	20.539	-13.249	1.00 50.76 1.00 53.57
ATOM	1510		LYS	A 444	9.166	20.064	-14.593	1.00 55.91
ATOM	1511		LYS	A 444	10.041		-15.193 -8.869	1.00 33.31
MOTA	1512			A 444	8.333 7.669	21.367 22.385		1.00 40.91
ATOM	1513			A 444 A 445	8.564	20.599		1.00 40.57
ATOM	1514 1515			A 445 A 445	8.100	20.993		1.00 40.29
MOTA	1515			A 445	8.291			
ATOM	1010							

			E 451	10 577	-5.846	1.00 43.76
MOTA	1517	CG LEU A 445	7.471	18.577	-5.224	1.00 46.83
MOTA	1518	CD1 LEU A 445	8.070	17.339	-5.405	1.00 45.67
MOTA	1519	CD2 LEU A 445	6.006	18.699 22.264	-5.932	1.00 39.05
MOTA	1520	C LEU A 445	8.802	23.148	-5.355	1.00 38.44
MOTA	1521	O LEU A 445	8.162	22.379	-6.131	1.00 37.84
ATOM	1522	N GLN A 446	10.113		-5.630	1.00 37.19
MOTA	1523	CA GLN A 446	10.804	23.553	-5.770	1.00 36.98
ATOM	1524	CB GLN A 446	12.322	23.443	-5.128	1.00 38.75
ATOM	1525	CG GLN A 446	13.058	24.617	-5.312	1.00 40.58
MOTA	1526	CD GLN A 446	14.563	24.588 24.583	-6.428	1.00 42.73
MOTA	1527	OE1 GLN A 446	15.065	24.503	-4.206	1.00 41.51
MOTA	1528	NE2 GLN A 446	15.284	24.808	-6.332	1.00 36.39
MOTA	1529	C GLN A 446	10.312	25.880	-5.715	1.00 35.15
MOTA	1530	O GLN A 446	10.218 10.037	24.680	-7.626	1.00 36.58
MOTA	1531	N GLN A 447	9.547	25.810	-8.415	1.00 37.09
MOTA	1532	CA GLN A 447	9.316	25.428	-9.872	1.00 37.88
MOTA	1533	CB GLN A 447	10.545	25.058		1.00 42.37
ATOM	1534	CG GLN A 447	10.176	24.683	-12.104	1.00 49.26
ATOM	1535	CD GLN A 447	9.144	25 147	-12.634	1.00 53.32
MOTA	1536	OE1 GLN A 447 NE2 GLN A 447	10.993	23.831	-12.729	1.00 52.11
ATOM	1537		8.231	26.343	-7.845	1.00 35.60
ATOM	1538		8.075	27.518	-7.726	1.00 33.62
ATOM	1539		7.305	25.461	-7.508	1.00 35.56
ATOM	1540	N LYS A 448 CA LYS A 448	6.055	25.897	-6.903	1.00 36.26
MOTA	1541	CB LYS A 448	5.125	24.707	-6.684	1.00 36.75
MOTA	1542 1543	CG LYS A 448	4.434	24.265	-7.968	1.00 41.05
MOTA	1544	CD LYS A 448	3.642	22.962	-7.752	1.00 45.62
ATOM ATOM	1545	CE LYS A 448	2.734	22.623	-8.941	1.00 47.75
ATOM	1546	NZ LYS A 448	1.655	21.655	-8.507	1.00 51.38
ATOM	1547	C LYS A 448	6.304	26.615	-5.584	1.00 35.43
ATOM	1548	O LYS A 448	5.762	27.697	-5.345	1.00 34.04
MOTA	1549	N ILE A 449	7.118	25.997	-4.720	1.00 35.23
ATOM	1550	CA ILE A 449	7.422	26.574	-3.428	1.00 35.08
ATOM	1551	CB ILE A 449	8.400	25,663	-2.647	1.00 35.31
MOTA	1552	CG1 ILE A 449	7.662	24.412	-2.135	1.00 34.62
ATOM	1553	CD1 ILE A 449	8.565	23.272	-1.666	1.00 35.68 1.00 34.70
MOTA	1554	CG2 ILE A 449	9.036	26.439	-1.508	1.00 34.70 1.00 35.67
MOTA	1555	C ILE A 449	8.009	27.950	-3.648	1.00 35.07
MOTA	1556	O ILE A 449	7.663	28.891	-2.954 -4.648	1.00 36.15
MOTA	1557	N GLN A 450	8.863	28.092 29.383	-4.898	1.00 37.22
ATOM	1558	CA GLN A 450	9.491	29.245	-5.929	1.00 37.71
ATOM	1559	CB GLN A 450	10.624 11.440	30.525	-6.143	1.00 39.93
MOTA	1560	CG GLN A 450	12.459	30.323	-7.271	1.00 44.24
MOTA	1561	CD GLN A 450	13.107	29.339	-7.409	1.00 46.56
ATOM	1562	OE1 GLN A 450 NE2 GLN A 450	12.603	31.421	-8.071	1.00 46.99
ATOM	1563		8.497	30.453	-5.351	1.00 37.23
MOTA	1564	450	8.668	31.629	-5.033	1.00 36.57
MOTA	1565 1566	O GLN A 450 N LEU A 451	7.460	30.067	-6.095	1.00 37.47
ATOM	1567	CA LEU A 451	6.491	31.055	-6.548	1.00 38.17
MOTA MOTA	1568	CB LEU A 451	5.602	30.496	-7.658	1.00 39.23
ATOM	1569	CG LEU A 451	6.299	30.228	-8.992	1.00 40.16
ATOM	1570		5.417	29.356	-9.874	1.00 42.60
ATOM	1571	CD2 LEU A 451	6.671		-9.709	1.00 40.87
MOTA	1572	C LEU A 451	5.675		-5.350	1.00 38.38
ATOM	1573	O LEU A 451	5.328			
ATOM	1574	N ALA A 452	5.396			
ATOM	1575	CA ALA A 452	4.683			
ATOM	1576	CB ALA A 452	4.352			
MOTA	1577	C ALA A 452	5.492			
MOTA	1578		4.960	32.541	-1.667 -2.302	
MOTA	1579		6.793			
MOTA	1580		7.650 9.078			
ATOM	1581		10.108			
MOTA	1582	CG LEU A 453	10.100	. 32.334		

	1502 /	CD1 LEU A 453	9.785	32.702	0.737	1.00 37.68
ATOM ATOM	1583 (1584 (CD2 LEU A 453	11.487	31.994	-0.924	1.00 39.28
ATOM		C LEU A 453	7.649	33.727	-1.936	1.00 41.01
ATOM		O LEU A 453	7.559	34.652	-1.143	1.00 40.74 1.00 43.21
MOTA	1587	N GLN A 454	7.784	33.912	-3.245	1.00 43.21
MOTA		CA GLN A 454	7.778	35.242 35.097	-3.857 -5.353	1.00 44.93
MOTA		CB GLN A 454	8.018 8.139	36.413	-6.092	1.00 47.00
MOTA		CG GLN A 454 CD GLN A 454	8.484	36.232	-7.549	1.00 50.13
MOTA		CD GLN A 454 OE1 GLN A 454	7.937	35.355	-8.224	1.00 51.04
ATOM ATOM		NE2 GLN A 454	9.397	37.062	-8.044	1.00 52.53
ATOM		C GLN A 454	6.438	35.937	-3.580	1.00 45.15
ATOM	-	O GLN A 454	6.385	37.105	-3.193	1.00 45.17 1.00 46.23
MOTA		N HIS A 455	5.363	35.186	-3.735 -3.418	1.00 40.23
MOTA		CA HIS A 455	4.029 3.064	35.654 34.479	-3.557	1.00 47.88
MOTA		CB HIS A 455	1.659	34.782	-3.164	1.00 50.63
MOTA	1599	CG HIS A 455 ND1 HIS A 455	0.939	35.826	-3.706	1.00 52.70
MOTA MOTA	1600 1601	CE1 HIS A 455	-0.272	35.843	-3.172	1.00 53.57
ATOM	1602	NE2 HIS A 455	-0.363	34.844	-2.309	1.00 53.78
MOTA	1603	CD2 HIS A 455	0.833	34.167	-2.283	1.00 52.74 1.00 48.21
ATOM	1604	C HIS A 455	3.974	36.276	-2.018 -1.852	1.00 48.21
MOTA	1605	O HIS A 455	3.561	37.425 35.544	-1.017	1.00 48.96
MOTA	1606	N VAL A 456	4.436 4.409	36.035	0.369	1.00 49.83
ATOM	1607	CA VAL A 456 CB VAL A 456	4.656	34.884	1.353	1.00 49.91
MOTA	1608 1609	CG1 VAL A 456	4.882	35.394	2.759	1.00 50.35
MOTA MOTA	1610	CG2 VAL A 456	3.498	33.899	1.325	1.00 50.07
ATOM	1611	C VAL A 456	5.437	37.101	0.684	1.00 50.39
ATOM	1612	O VAL A 456	5.262	37.865	1.625 -0.062	1.00 50.47 1.00 51.74
MOTA	1613	N LEU A 457	6.529 7.538	37.119 38.140	0.062	1.00 53.74
MOTA	1614	CA LEU A 457	8.801	37.829	-0.648	1.00 53.04
ATOM	1615	CB LEU A 457 CG LEU A 457	9.664	36.711	-0.065	1.00 52.30
ATOM ATOM	1616 1617	CD1 LEU A 457	10.705	36.350	-1.081	1.00 51.56
ATOM	1618	CD2 LEU A 457	10.296	37.172	1.254	1.00 50.93
ATOM	1619	C LEU A 457	6.979	39.480	-0.294	1.00 55.43 1.00 54.68
ATOM	1620	O LEU A 457	7.071	40.456 39.516	0.437 -1.480	1.00 54.68 1.00 58.58
MOTA	1621	N GLN A 458	6.372 5.836	40.764	-2.020	1.00 61.31
ATOM	1622	CA GLN A 458 CB GLN A 458	5.596	40.661	-3.538	1.00 61.66
MOTA	1623 1624	CB GLN A 458 CG GLN A 458	4.556	39.646	-4.008	1.00 63.40
MOTA MOTA	1625	CD GLN A 458	4.816	39.189	-5.449	1.00 65.86
MOTA	1626	OE1 GLN A 458	5.793	39.622	-6.069	1.00 67.19
MOTA	1627	NE2 GLN A 458	3.949	38.313	-5.978	1.00 66.76 1.00 63.26
MOTA	1628	C GLN A 458	4.591 4.268	41.256 42.434	-1.265 -1.282	1.00 63.20
MOTA	1629	O GLN A 458	3.929	40.359		
MOTA	1630	N LYS A 459 CA LYS A 459	2.770	40.732	0.228	1.00 67.66
ATOM ATOM	1631 1632	CA LYS A 459 CB LYS A 459	2.241		0.894	1.00 67.68
MOTA	1633	CG LYS A 459	1.061	39.617	1.825	1.00 67.62
ATOM	1634	CD LYS A 459	0.638	38.243	2.332	1.00 67.67 1.00 67.92
MOTA	1635	CE LYS A 459	-0.042		1.241 1.597	1.00 68.58
MOTA	1636	NZ LYS A 459	-0.160 3.116		1.290	1.00 69.97
MOTA	1637	C LYS A 459 O LYS A 459	2.285		1.648	1.00 70.29
MOTA	1638 1639	O LYS A 459 N ASN A 460	4.361	41.747	1.755	1.00 72.42
MOTA MOTA	1640	CA ASN A 460	4.802	42.571	2.871	
ATOM	1641	CB ASN A 460	5.508		3.896	
MOTA	1642	CG ASN A 460	4.624		4.390	
MOTA	1643	OD1 ASN A 460	3.556		4.964 4.165	
MOTA	1644	ND2 ASN A 460	5.071 5.731		2.501	1.00 76.15
MOTA	1645	C ASN A 460 O ASN A 460	5.676			1.00 76.33
MOTA MOTA	1646 1647	N HIS A 461	6.582	43.529	1.496	1.00 78.30
ATOM	1648	CA HIS A 461	7.564	44.550	1.141	1.00 79.89

		1 200 1 00 00 20
T COM	1649 CB HIS A 461	8.846 44.307 1.932 1.00 80.20
ATOM		8.629 44.208 3.407 1.00 81.84
ATOM		8 597 45 312 4.234 1.00 84.02
MOTA		8 377 44 919 5.478 1.00 84.23
MOTA	1652 CE1 HIS A 461	8.253 43.603 5.484 1.00 83.90
MOTA	1653 NE2 HIS A 461	0.233 43.000
MOTA	1654 CD2 HIS A 461	0.400 43.400 00 00
ATOM	1655 C HIS A 461	7.507 44.000
ATOM	1656 O HIS A 461	3.007
ATOM	1657 N ARG A 462	6.912 44.841 -1.191 1.00 82.27
		7.194 45.051 -2.605 1.00 83.28
ATOM	150	5 903 45 330 -3.393 1.00 83.78
MOTA		5 303 44 070 -4.042 1.00 85.00
MOTA		3 898 44 230 -4.665 1.00 86.49
MOTA	1661 CD ARG A 462	3.505 43.033 -5.417 1.00 87.52
ATOM	1662 NE ARG A 462	2.281 42.778 -5.865 1.00 88.16
MOTA	1663 CZ ARG A 462	2.201 12111 1 00 00 54
MOTA	1664 NH1 ARG A 462	1.200 1 00 07 06
ATOM	1665 NH2 ARG A 462	2.000 12.000
ATOM	1666 C ARG A 462	0.101 100 100 00 72
MOTA	1667 O ARG A 462	0.544
	1668 N GLU A 463	8.649 46.649 -1.506 1.00 83.89
MOTA	1669 CA GLU A 463	9.624 47.723 -1.335 1.00 83.96
MOTA	_ 4.55	9 947 47 970 0.156 1.00 84.16
MOTA		10 746 46 939 0.821 1.00 84.97
MOTA	4.55	10 741 47 071 2.326 1.00 85.96
MOTA		10 286 48 126 2.808 1.00 87.00
MOTA	1673 OE1 GLU A 463	10.200 1 00 06 60
MOTA	1674 OE2 GLU A 463	11.100 10.00 A7
MOTA	1675 C GLU A 463	10.500 27.121
MOTA	1676 O GLU A 463	11.752 10.000 10.00 00 00
MOTA	1677 N ASP A 464	11.2/4 10.000 00 00
ATOM	1678 CA ASP A 464	12.332 13.07
ATOM	1679 CB ASP A 464	13.370 13.37
ATOM	1680 CG ASP A 464	11.100
MOTA	1681 OD1 ASP A 464	13.981 47.814 -1.626 1.00 82.80
	1682 OD2 ASP A 464	14.766 46.795 0.079 1.00 82.96
MOTA	1683 C ASP A 464	12.251 44.380 -3.467 1.00 81.10
ATOM	4.6.4	11 103 44 121 -3.868 1.00 81.10
MOTA	^	12 205 43 599 -3.701 1.00 /9.69
MOTA		13 210 42 292 -4.339 1.00 78.42
MOTA		14 125 41 358 -3.567 1.00 77.09
MOTA	1687 C GLY A 465	15.055 40.776 -4.128 1.00 76.83
MOTA	1688 O GLY A 465	13.839 41.229 -2.269 1.00 75.34
MOTA	1689 N ILE A 466	14.687 40.507 -1.318 1.00 73.67
MOTA	1690 CA ILE A 466	14.007
ATOM	1691 CB ILE A 466	TT-170 1 00 MA 10
MOTA	1692 CG1 ILE A 466	10.704 12.000
MOTA	1693 CD1 ILE A 466	13.210 12.110 1 00 74 24
ATOM	1694 CG2 ILE A 466	13.312 10.110
MOTA	1695 C ILE A 466	14.750 55.020
ATOM	1696 O ILE A 466	13.002 1 00 60 76
MOTA	1697 N LEU A 467	13.860 38.535 -2.425 1.00 69.76
	1698 CA LEU A 467	13.872 37.134 -2.791 1.00 68.62
MOTA	1699 CB LEU A 467	12.849 36.853 -3.889 1.00 68.53
ATOM		10 700 35 400 -4.353 1.00 08.8/
ATOM		12 138 34 497 -3.294 1.00 69.10
MOTA	1701 CD1 LEU A 467	11 854 35 347 -5.579 1.00 /0.46
MOTA	1702 CD2 LEU A 467	15 273 36 746 -3.247 1.00 67.31
MOTA	1703 C LEU A 467	15 733 35 642 -2.961 1.00 67.18
MOTA	1704 O LEU A 467	15.753 33.642 2.5934 1.00 65.58
MOTA		1 450 1 00 64 62
MOTA	1706 CA THR A 468	17.203 37.002
ATOM	1707 CB THR A 468	17.000
ATOM	1708 OG1 THR A 468	17.70= 3300
MOTA	1709 CG2 THR A 468	10.031 30.120
MOTA	1710 C THR A 468	10.310 37.307
ATOM	1711 O THR A 468	13.200 30.000
MOTA		10.213 30.31
MOTA		15.000 50.507
MOTA	7770 7 460	18.797 39.647 -0.484 1.00 62.13
AIOH		

		19.486	39.829	0.860	1.00 62.89
ATOM	1715 CG LYS A 469 1716 CD LYS A 469	19.456	41.310	1.276	1.00 64.52
ATOM	460	19.505	41.608	2.756	1.00 65.74
ATOM		18.942	42.951	3.178	1.00 66.28
ATOM	1718 NZ LYS A 469 1719 C LYS A 469	18.854	37.133	-0.355	1.00 59.69
MOTA	1719 C BIS R 409	19.766	36.645	0.317	1.00 59.53
MOTA	1721 N LEU A 470	17.627	36.633	-0.360	1.00 57.33
ATOM ATOM	1722 CA LEU A 470	17.292	35.439	0.387	1.00 56.01
ATOM	1723 CB LEU A 470	15.771		0.527	1.00 55.44
ATOM	1724 CG LEU A 470	15.242	34.622	1.770	1.00 54.97
MOTA	1725 CD1 LEU A 470	15.881	35.167	3.018	1.00 54.08 1.00 56.05
ATOM	1726 CD2 LEU A 470	13.721	34.701	1.859 -0.331	1.00 55.43
ATOM	1727 C LEU A 470	17.861	34.213	0.281	1.00 54.90
MOTA	1728 O LEU A 470	18.522	33.382 34.111	-1.635	1.00 54.68
MOTA	1729 N ILE A 471	17.624 18.120	32.986	-2.412	1.00 54.43
MOTA	1730 CA ILE A 471	17.538	33.016	-3.836	1.00 54.76
MOTA	1731 CB ILE A 471 1732 CG1 ILE A 471	16.097	32.526	-3.792	1.00 55.40
ATOM	1732 CG1 ILE A 471 1733 CD1 ILE A 471	15.438	32.478	-5.119	1.00 56.34
MOTA	1734 CG2 ILE A 471	18.372	32.144	-4.798	1.00 55.26
ATOM ATOM	1735 C ILE A 471	19.631	33.016	-2.433	1.00 53.73
ATOM	1736 O ILE A 471	20.281	31.996	-2.616	1.00 53.69
MOTA	1737 N CYS A 472	20.189	34.198	-2.239	1.00 52.86 1.00 52.63
ATOM	1738 CA CYS A 472	21.625	34.347	-2.120	1.00 52.63 1.00 52.92
MOTA	1739 CB CYS A 472	21.979	35.829	-1.990 -3.399	1.00 58.34
MOTA	1740 SG CYS A 472	22.874	36.495 33.604	-0.886	1.00 50.97
MOTA	1741 C CYS A 472	22.157 23.290	33.104	-0.901	1.00 50.65
MOTA	1742 O CYS A 472 1743 N LYS A 473	21.348	33.555	0.179	1.00 48.54
ATOM		21.758	32.936	1.439	1.00 47.29
MOTA	1744 CA LYS A 473 1745 CB LYS A 473	20.754	33.227	2.562	1.00 47.39
MOTA MOTA	1745 CB HIS A 473	20.619	34.712	2.930	1.00 49.59
ATOM	1747 CD LYS A 473	21.832	35.243	3.708	1.00 52.10
ATOM	1748 CE LYS A 473	22.062	36.733	3.414	1.00 54.59
MOTA	1749 NZ LYS A 473	23.470	37.017	2.981	1.00 56.43 1.00 45.26
ATOM	1750 C LYS A 473	21.875	31.450	1.277 1.995	1.00 45.25
ATOM	1751 O LYS A 473	22.631	30.804 30.919	0.327	1.00 43.23
MOTA	1752 N VAL A 474	21.122 21.136	29.518	0.102	1.00 42.19
ATOM	1753 CA VAL A 474 1754 CB VAL A 474	20.387	29.116	-1.145	1.00 42.59
MOTA		20.645	27.663	-1.449	1.00 42.42
MOTA MOTA	1755 CG1 VAL A 474 1756 CG2 VAL A 474	18.910	29.383	-0.957	1.00 42.39
MOTA	1757 C VAL A 474	22.546	29.055	-0.055	1.00 41.04
MOTA	1758 O VAL A 474	22.919	28.042	0.503	1.00 39.72
ATOM	1759 N SER A 475	23.345	29.780	-0.812	1.00 39.27 1.00 38.63
ATOM	1760 CA SER A 475	24.718	29.353	-0.979 -2.070	1.00 38.92
MOTA	1761 CB SER A 475	25.402	30.157	-2.029	1.00 40.43
MOTA	1762 OG SER A 475	26.788 25.490	29.921 29.483	0.336	1.00 37.50
ATOM	1763 C SER A 475 1764 O SER A 475	26.430	28.759	0.576	1.00 36.17
ATOM		25.118	30.425	1.192	1.00 36.92
MOTA MOTA	1765 N THR A 476 1766 CA THR A 476	25.854		2.443	1.00 36.78
MOTA	1767 CB THR A 476	25.460	31.898	3.133	1.00 37.27
MOTA	1768 OG1 THR A 476	25.293	32.946	2.166	1.00 39.90
ATOM	1769 CG2 THR A 476	26.543		4.043	1.00 37.41 1.00 36.02
ATOM	1770 C THR A 476	25.588		3.378 4.084	
ATOM	1771 O THR A 476	26.489		3.360	
ATOM	1772 N LEU A 477	24.355 23.939		4.200	
ATOM		22.457		4.019	1.00 35.72
MOTA		21.480		4.875	1.00 35.56
ATOM ATOM	A	20.057		4.321	
ATOM	477	21.584	27.800		
MOTA	1778 C LEU A 477	24.670			
MOTA	1779 O LEU A 477	24.966			
ATOM		24.941	26.311	2.610	1.00 33.90

WO 03/093312 PCT/EP03/04433

ATOM	1781	CA ARG A 478	25.659	25.124	2.183	1.00 36.68
	1782	CB ARG A 478	25.606	24.989	0.666	1.00 37.49
ATOM	1783	CG ARG A 478	24.216	24.645	0.185	1.00 39.62
MOTA		·	24.110	24.375	-1.293	1.00 41.13
MOTA	1784		22.727	24.112	-1.658	1.00 42.25
MOTA	1785		22.342	23.503	-2.763	1.00 43.78
MOTA	1786	CZ ARG A 478	23.246	23.088	-3.641	1.00 45.06
MOTA	1787	NH1 ARG A 478		23.312	-3.003	1.00 42.39
ATOM	1788	NH2 ARG A 478	21.045	25.179	2.666	1.00 36.22
MOTA	1789	C ARG A 478	27.093		3.056	1.00 36.31
ATOM	1790	O ARG A 478	27.655	24.170	2.645	1.00 35.43
MOTA	1791	N ALA A 479	27.690	26.361	3.144	1.00 34.83
ATOM	1792	CA ALA A 479	29.045	26.502		1.00 34.35
ATOM	1793	CB ALA A 479	29.634	27.829	2.714	1.00 34.50
ATOM	1794	C ALA A 479	29.029	26.382	4.674	1.00 33.03
MOTA	1795	O ALA A 479	29.923	25.803	5.254	1.00 33.03
ATOM	1796	N LEU A 480	28.011	26.924	5.330	1.00 34.39 1.00 35.19
ATOM	1797	CA LEU A 480	27.931	26.756	6.768	
ATOM	1798	CB LEU A 480	26.787	27.598	7.348	1.00 35.91
ATOM	1799	CG LEU A 480	26.747	27.805	8.845	1.00 35.84
ATOM	1800	CD1 LEU A 480	28.051	28.355	9.382	1.00 37.04
ATOM	1801	CD2 LEU A 480	25.590	28.734	9.189	1.00 36.87
ATOM	1802	C LEU A 480	27.787	25.276	7.138	1.00 35.48
	1803	O LEU A 480	28.525	24.768	7.999	1.00 36.43
MOTA	1804	N CYS A 481	26.886	24.557	6.482	1.00 34.90
ATOM	1805	CA CYS A 481	26.721	23.150	6.768	1.00 35.75
ATOM	1805	CB CYS A 481	25.408	22.617	6.151	1.00 35.51
MOTA		SG CYS A 481	23.970	23.492	6.880	1.00 39.57
MOTA	1807		27.955	22.339	6.343	1.00 35.95
MOTA	1808	404	28.248	21.278	6.914	1.00 35.58
ATOM	1809	100	28.690	22.846	5.359	1.00 35.86
MOTA	1810		29.909	22.197	4.922	1.00 35.86
ATOM	1811		30.978	22.309	5.983	1.00 35.56
MOTA	1812	400	31.689	21.375	6.268	1.00 35.07
MOTA	1813		31.111	23.464	6.587	1.00 36.33
ATOM	1814		32.099	23.572	7.623	1.00 37.63
ATOM	1615	CA ARG A 483	32.250	25.000	8.046	1.00 38.73
MOTA	1816	CB ARG A 483	32.770	25.873	6.900	1.00 43.48
MOTA	1817	CG ARG A 483	34.089	26.567	7.220	1.00 48.75
MOTA	1818	CD ARG A 483	34.129	27.928	6.699	1.00 52.27
MOTA	1819	NE ARG A 483	34.148	29.016	7.463	1.00 56.41
MOTA	1820	CZ ARG A 483	34.138	28.914	8.793	1.00 55.60
ATOM	1821	NH1 ARG A 483	34.177	30.224	6.894	1.00 59.68
MOTA	1822	NH2 ARG A 483	31.767	22.661	8.813	1.00 37.14
MOTA	1823	C ARG A 483	32.662	22.026	9.401	1.00 36.58
MOTA	1824	O ARG A 483	30.486	22.567	9.161	1.00 36.27
ATOM	1825	N HIS A 484	30.119	21.712	10.270	1.00 35.26
MOTA	1826	CA HIS A 484	28.615	21.655	10.449	1.00 34.25
MOTA	1827	CB HIS A 484	28.161	20.599	11.394	1.00 31.44
MOTA	1828	CG HIS A 484	27.481	19.481	10.975	1.00 26.89
ATOM	1829	ND1 HIS A 484	27.431	18.740	12.032	1.00 29.68
MOTA	1830	CE1 HIS A 484		19.307	13.111	1.00 26.36
MOTA	1831	NE2 HIS A 484	27.689	20.484	12.740	1.00 29.62
ATOM	1832	CD2 HIS A 484	28.293	20.333	10.013	1.00 36.35
ATOM	1833	C HIS A 484	30.656	19.740	10.893	1.00 35.93
MOTA	1834		31.264		8.805	1.00 38.13
MOTA	1835		30.457	19.818 18.466	8.520	1.00 39.75
ATOM	1836		30.881		7.111	1.00 40.58
ATOM	1837		30.421	18.032	7.111	1.00 42.13
MOTA	1838	OG1 THR A 485	29.011	17.726	6.702	
MOTA	1839		31.050	16.685	8.663	
ATOM	1840	C THR A 485	32.404		9.092	
ATOM	1841	O THR A 485	32.903	17.312	8.297	
MOTA	1842		33.136		8.343	
MOTA	1843	CA GLU A 486	34.583		7.597	
MOTA	1844	CB GLU A 486	35.200		6.080	
MOTA	1845		35.297		5.215	
MOTA	1846	CD GLU A 486	35.265	21.3//	J. 213	

						4 00 50 10
MOTA	1847	OE1 GLU A 486	34.972	21.411	4.013	1.00 50.12
ATOM	1848	OE2 GLU A 486	35.538	22.715	5.690	1.00 50.93
MOTA		C GLU A 486	35.048	19.311	9.775	1.00 40.94
MOTA	1850	O GLU A 486	35.970	18.573	10.146	1.00 40.53
ATOM	1851	N LYS A 487	34.445	20.161	10.584	1.00 39.75
MOTA	1852	CA LYS A 487	34.828	20.215	11.976	1.00 38.97
ATOM	1853	CB LYS A 487	34.122	21.369	12.697	1.00 39.27
	1854	CG LYS A 487	34.760	22.719	12.395	1.00 42.48
MOTA MOTA	1855	CD LYS A 487	36.275	22.575	12.241	1.00 45.26
ATOM	1856	CE LYS A 487	36.953	23.908	12.119	1.00 47.44
ATOM	1857	NZ LYS A 487	37.048	24.550	13.468	1.00 50.31
MOTA	1858	C LYS A 487	34.509	18.896	12.637	1.00 38.04
ATOM	1859	O LYS A 487	35.306	18.390	13.405	1.00 37.61
ATOM	1860	N LEU A 488	33.354	18.329	12.317	1.00 37.23
ATOM	1861	CA LEU A 488	32.937	17.098	12.946	1.00 37.18 1.00 36.30
ATOM	1862	CB LEU A 488	31.502	16.755	12.561	1.00 36.30
ATOM	1863	CG LEU A 488	31.030	15.382	12.993	1.00 30.23
ATOM	1864	CD1 LEU A 488	31.060	15.184	14.496	1.00 37.46
ATOM	1865	CD2 LEU A 488	29.636	15.172	12.465	1.00 37.99
ATOM	1866	C LEU A 488	33.885	15.955	12.593 13.466	1.00 37.01
ATOM	1867	O LEU A 488	34.238	15.147	11.317	1.00 37.01
ATOM	1868	N MET A 489	34.263	15.851	10.932	1.00 40.07
MOTA	1869	CA MET A 489	35.240	14.828	9.409	1.00 40.81
MOTA	1870	CB MET A 489	35.412	14.694	8.704	1.00 44.15
MOTA	1871	CG MET A 489	34.178	14.171 12.913	9.641	1.00 54.88
ATOM	1872	SD MET A 489	33.194	11.239	9.132	1.00 55.79
ATOM	1873	CE MET A 489	33.908	15.107	11.636	1.00 39.24
MOTA	1874	C MET A 489	36.572 37.216	14.197	12.086	1.00 38.99
ATOM	1875	O MET A 489	36.960	16.356	11.813	1.00 39.22
MOTA	1876	N ALA A 490	38.226	16.606	12.512	1.00 39.46
ATOM	1877	CA ALA A 490 CB ALA A 490	38.623	18.062	12.412	1.00 38.63
MOTA	1878		38.152	16.166	13.997	1.00 40.06
ATOM	1879		39.131	15.669	14.568	1.00 40.68
ATOM	1880		36.979	16.351	14.602	1.00 39.40
ATOM	1881	N PHE A 491 CA PHE A 491	36.756	15.996	15.982	1.00 38.41
MOTA	1882 1883	CB PHE A 491	35.449	16.640	16.482	1.00 37.82
MOTA	1884	CG PHE A 491	35.055	16.218	17.871	1.00 34.23
MOTA MOTA	1885	CD1 PHE A 491	35.515	16.907	18.979	1.00 31.46
ATOM	1886	CE1 PHE A 491	35.168	16.507	20.263	1.00 31.14
ATOM	1887	CZ PHE A 491	34.329	15.411	20.445	1.00 29.45
ATOM	1888	CE2 PHE A 491	33.873	14.724	19.340	1.00 32.47
MOTA	1889	CD2 PHE A 491	34.233	15.134	18.058	1.00 31.03 1.00 39.01
ATOM	1890	C PHE A 491	36.695	14.484	16.112	1.00 39.01
ATOM	1891	O PHE A 491	37.183	13.910	17.079	1.00 38.94
ATOM	1892	N LYS A 492	36.077	13.831	15.153 15.226	1.00 40.55
ATOM	1893	CA LYS A 492	35.941	12.401		1.00 40.93
MOTA	1894	CB LYS A 492	34.934	11.958 10.473	14.192 14.114	1.00 42.40
MOTA	1895	CG LYS A 492	34.730	10.473	13.098	1.00 44.01
ATOM	1896	CD LYS A 492	33.670		12.999	1.00 44.96
MOTA	1897	CE LYS A 492	33.493		12.044	1.00 47.85
MOTA	1898	NZ LYS A 492	32.414 37.283	11.668	15.031	1.00 41.46
MOTA	1899	C LYS A 492	37.425		15.389	1.00 41.69
MOTA	1900	O LYS A 492	38.275		14.476	
MOTA	1901	N ALA A 493 CA ALA A 493	39.570		14.290	1.00 43.19
ATOM	1902	400	40.374		13.226	1.00 43.14
MOTA	1903		40.340		15.612	1.00 43.40
MOTA	1904	400	41.244		15.802	1.00 44.12
MOTA	1905 1906	O ALA A 493 N ILE A 494	39.979			1.00 42.66
MOTA	1907	CA ILE A 494	40.651		17.806	
ATOM ATOM	1908	CB ILE A 494	40.873	14.048	18.163	
ATOM	1909		41.824			
ATOM			41.756			
ATOM		CG2 ILE A 494	41.451	14.167	19.560	
ATOM			39.882	11.920	18.942	1.00 41.61
	. –					

			40 405	11.551	19.953	1.00 41.78
MOTA	1913	O ILE A 494	40.485 38.566	11.796	18.796	1.00 40.39
MOTA	1914	N TYR A 495	37.722	11.225	19.830	1.00 39.98
ATOM	1915	CA TYR A 495		12.324	20.513	1.00 39.79
MOTA	1916	CB TYR A 495	36.916	13.430	21.115	1.00 38.81
ATOM	1917	CG TYR A 495	37.731	14.585	20.415	1.00 38.27
MOTA	1918	CD1 TYR A 495	37.949	15.600	20.932	1.00 38.45
ATOM	1919	CE1 TYR A 495	38.685	15.508	22.194	1.00 39.44
MOTA	1920	CZ TYR A 495	39.209	16.582	22.669	1.00 40.01
MOTA	1921	OH TYR A 495	39.947	14.366	22.941	1.00 38.56
ATOM	1922	CE2 TYR A 495	39.013	13.329	22.402	1.00 38.69
MOTA	1923	CD2 TYR A 495	38.260	10.209	19.257	1.00 40.43
MOTA	1924	C TYR A 495	36.747 35.548	10.209	19.483	1.00 40.56
MOTA	1925	O TYR A 495		9.201	18.567	1.00 40.98
MOTA	1926	N PRO A 496	37.255	8.261	17.871	1.00 40.62
ATOM	1927	CA PRO A 496	36.379	7.229	17.288	1.00 41.12
MOTA	1928	CB PRO A 496	37.344 38.747	7.789	17.496	1.00 41.49
ATOM	1929	CG PRO A 496	38.747	-8.848	18.486	1.00 40.68
MOTA	1930	CD PRO A 496	35.392	7.567	18.796	1.00 40.79
MOTA	1931	C PRO A 496	34.263	7.261	18.404	1.00 41.69
MOTA	1932	O PRO A 496	35.814	7.254	20.008	1.00 40.89
MOTA	1933	N ASP A 497	34.937	6.528	20.913	1.00 40.80
MOTA	1934	CA ASP A 497	35.745	5.792	21.988	1.00 41.84
MOTA	1935	CB ASP A 497	36.300	4.475	21.485	1.00 45.64
MOTA	1936	CG ASP A 497	36.821	3.696	22.320	1.00 53.60
ATOM	1937	OD1 ASP A 497	36.249	4.124	20.282	1.00 48.70
MOTA	1938	OD2 ASP A 497	33.902	7.409	21.579	1.00 39.07
MOTA	1939	C ASP A 497	32.847	6.919	21.956	1.00 38.09
MOTA	1940	O ASP A 497	34.211	8.697	21.744	1.00 38.14
MOTA	1941	N ILE A 498	33.230	9.640	22.273	1.00 37.33
MOTA	1942	CA ILE A 498	33.864	11.039	22.491	1.00 38.00
ATOM	1943	CB ILE A 498	34.902	11.018	23.627	1.00 39.27
MOTA	1944	CG1 ILE A 498 CD1 ILE A 498	34.375	10.559	24.947	1.00 40.90
MOTA	1945		32.797	12.090	22.770	1.00 37.86
MOTA	1946		32.092	9.696	21.272	1.00 36.02
ATOM	1947	400	30.929	9.572	21.625	1.00 35.72
MOTA	1948	400	32.429	9.814	20.002	1.00 35.39
MOTA	1949	- 400	31.400	9.915	18.994	1.00 35.49
MOTA	1950 1951	CA VAL A 499 CB VAL A 499	31.969	10.182	17.580	1.00 34.87
MOTA		CG1 VAL A 499	30.868	10.168	16.543	1.00 34.58
MOTA	1952 1953	CG2 VAL A 499	32.686	11.485	17.542	1.00 34.93
MOTA	1954	C VAL A 499	30.598	8.647	18.975	1.00 35.88
MOTA	1955	0 VAL A 499	29.384	8.684	18.933	1.00 36.02
MOTA MOTA	1956	N ARG A 500	31.278	7.515	19.004	1.00 36.41
ATOM	1957	CA ARG A 500	30.600	6.237	18.880	1.00 36.86
ATOM	1958	CB ARG A 500	31.629		18.714	1.00 37.54
ATOM	1959	CG ARG A 500	31.058	3.739	18.596	1.00 41.50
ATOM	1960	CD ARG A 500	32.137	2.639	18.598	1.00 46.56
ATOM	1961	NE ARG A 500	31.814		19.576	1.00 51.65
ATOM	1962	CZ ARG A 500	32.514		20.688	1.00 52.82
ATOM	1963	NH1 ARG A 500	33.613	2.013	20.978	1.00 53.74
MOTA	1964	NH2 ARG A 500	32.117	0.370	21.508	1.00 54.03 1.00 36.07
ATOM	1965	C ARG A 500	29.724		20.066	
MOTA	1966	O ARG A 500	28.570		19.884	
MOTA	1967	N LEU A 501	30.247	6.133	21.277	
MOTA	1968	CA LEU A 501	29.493	5.780	22.495	
ATOM	1969	CB LEU A 501	30.444			
ATOM	1970	CG LEU A 501	31.187			
MOTA	1971	CD1 LEU A 501	32.025			
MOTA	1972		30.219			
ATOM	1973		28.609			
ATOM	1974		27.660			
MOTA	1975		28.891 28.121			
MOTA	1976		29.049			
MOTA	1977		29.690			
MOTA	1978	CG HIS A 502	29.030	, 0.,,,		

			0.440	26.515	1.00 34.45
ATOM	1979 ND1 HIS A 502	28.998	8.440 7.616	27.175	1.00 33.23
ATOM	1980 CE1 HIS A 502	29.796	7.610	26.582	1.00 32.06
ATOM	1981 NE2 HIS A 502	30.978	8.457		1.00 32.50
ATOM	1982 CD2 HIS A 502	30.940	10.237	22.575	1.00 31.35
ATOM	1983 C HIS A 502	2 27.392	11.084	23.064	1.00 32.31
ATOM	1984 O HIS A 50	2 26.671 3 27.572	10.171	21.269	1.00 30.30
MOTA	1985 N PHE A 50		11.071	20.401	1.00 29.71
MOTA	1986 CA PHE A 50		11.366	19.123	1.00 28.59
MOTA	1987 CB PHE A 50		12.527	19.253	1.00 27.67
MOTA	1988 CG PHE A 50		12.774	20.443	1.00 28.62
MOTA	1989 CD1 PHE A 50 1990 CE1 PHE A 50		13.869	20.575	1.00 24.57
MOTA			14.715	19.523	1.00 23.93
MOTA		-	14.481	18.322	1.00 27.80
MOTA			13.402	18.194	1.00 27.49
MOTA	1993 CD2 PHE A 50 1994 C PHE A 50		10.483	20.086	1.00 29.88
MOTA	1995 O PHE A 50	3 25.301	9.290	20.004	1.00 29.58
MOTA MOTA	1996 N PRO A 50	4 24.472	11.327	19.887	1.00 30.28
ATOM	1997 CA PRO A 50	4 23.131	10.838	19.561	1.00 30.42 1.00 30.02
ATOM	1998 CB PRO A 50	4 22.305	12.107	19.435	1.00 30.52
MOTA	1999 CG PRO A 50	4 23.129	13.163	20.095	1.00 30.30
ATOM	2000 CD PRO A 50	4 24.559	12.793	19.900 18.232	1.00 30.68
ATOM	2001 C PRO A 50	23.112	10.094 10.533	17.261	1.00 29.79
MOTA	2002 O PRO A 50	23.698	8.973	18.199	1.00 31.99
MOTA	2003 N PRO A 50		8.126	16.997	1.00 32.55
ATOM	2004 CA PRO A 50		7.055	17.397	1.00 32.91
MOTA	2005 CB PRO A 50		6.943	18.876	1.00 33.39
MOTA	2006 CG PRO A 50 2007 CD PRO A 50		8.384	19.347	1.00 32.17
MOTA			8.820	15.736	1.00 32.64
MOTA	2008 C PRO A 50 2009 O PRO A 50		8.540	14.662	1.00 33.22
ATOM ATOM	2010 N LEU A 50		9.709	15.843	1.00 32.69
ATOM	2011 CA LEU A 50	06 20.388	10.427	14.673	1.00 32.07 1.00 32.44
ATOM	2012 CB LEU A 5	06 19.117	11.204	15.015	1.00 32.44
ATOM	2013 CG LEU A 5	06 18.566	12.012	13.840 12.722	1.00 33.03
MOTA	2014 CD1 LEU A 5	06 18.156	11.092	14.302	1.00 33.49
ATOM	2015 CD2 LEU A 5	06 17.398	12.836 11.369	14.091	1.00 32.28
ATOM	2016 C LEU A 5	06 21.425 06 21.491	11.528	12.893	1.00 32.61
ATOM	2017 O LEU A 5		12.012	14.949	1.00 32.83
MOTA	2018 N TYR A 5 2019 CA TYR A 5		12.879	14.533	1.00 32.73
MOTA			13.589	15.762	1.00 32.18
ATOM	2020 CB TYR A 5 2021 CG TYR A 5		14.643	15.516	1.00 30.21
MOTA MOTA	2021 CG TIR N 5	07 24.733	15.980		1.00 27.51
MOTA	2023 CE1 TYR A 5	07 25.715			1.00 28.26 1.00 29.93
MOTA	2024 CZ TYR A 5	07 27.020			1.00 29.93 1.00 30.78
MOTA	2025 OH TYR A 5	07 28.032			1.00 28.89
ATOM	2026 CE2 TYR A 5	27.336		15.239 15.423	1.00 29.57
MOTA	2027 CD2 TYR A 5	26.365			
MOTA	2028 C TYR A 5	507 24.405 507 24.928			1.00 32.52
MOTA	2029 O TYR A 5				1.00 35.19
MOTA					1.00 36.84
MOTA				14.548	
MOTA		26.837	8.988		
MOTA MOTA		508 27.446	7.686	16.296	
ATOM	2035 CE LYS A 5	508 26.536			
ATOM	2036 NZ LYS A	508 27.053		17.721	
ATOM	2037 C LYS A	508 25.165			
ATOM	2038 O LYS A	508 25.908			
ATOM		509 23.893 509 23.313			1.00 39.31
ATOM					1.00 39.58
ATOM	and or other			2 11.815	1.00 44.44
ATOM				4 11.993	1.00 48.40
ATOM ATOM	OTIT 3				1.00 52.15
AION	2011 322				

ATOM		OE2 G	LU A	509	19.285 23.333	7.028 9.841	11.285 9.937	1.00 50.58 1.00 39.53
MOTA		C G O G	LU A	509 509	23.504	9.571	8.745	1.00 39.45
MOTA		N I	EU A	510	23.126	11.083	10.379	1.00 39.18
MOTA MOTA		CA I	EU A	510	23.067	12.201	9.456	1.00 39.07
ATOM		CB I	EU A	510	22.226	13.338	10.040	1.00 39.33 1.00 39.95
ATOM	2051	CG I	EU A	510	20.725	13.091	10.200	1.00 39.93
ATOM	2052	CD1 I	EU A	510	20.091	14.296	10.800 8.899	1.00 40.94
ATOM			EU A	510	20.058	12.768 12.783	9.030	1.00 38.89
MOTA		_	EU A	510	24.401 24.503	13.334	7.943	1.00 39.03
ATOM		O I	EU A PHE A	510	25.427	12.680	9.854	1.00 38.62
ATOM		N I	PHE A	511	26.619	13.464	9.591	1.00 38.51
MOTA	2057 2058	CA I	PHE A	511	26.736	14.569	10.646	1.00 38.47
MOTA MOTA	2059	CG I	PHE A	511	25.542	15.483	10.711	1.00 39.17 1.00 37.90
MOTA	2060	CD1	PHE A	511	24.848	15.663	11.910 11.985	1.00 37.30
ATOM	2061	CE1	PHE A	511	23.762	16.508 17.165	10.866	1.00 37.10
MOTA	2062	CZ	PHE A	511	23.324 24.005	16.998	9.653	1.00 39.88
MOTA	2063	CE2	PHE A	211	25.113	16.167	9.587	1.00 40.32
MOTA	2064	CD2	PHE A	511	27.915	12.682	9.565	1.00 38.68
MOTA	2065 2066	o :	PHE A	511	28.923	13.297	9.211	1.00 38.22
ATOM ATOM	2067	OXT	PHE A	511	27.963	11.489	9.895	1.00 39.77 1.00 40.20
MOTA	2068	C65	CHS L	1	29.670	21.352	16.280 16.502	1.00 40.20
ATOM	2069	C63	CHS L	1	28.173	21.713 20.583	17.354	1.00 36.38
MOTA	2070	C69	CHS L	1	27.552 28.076	23.102	17.181	1.00 33.50
ATOM	2071	C60	CHS L CHS L	1 1	26.755	23.921	17.026	1.00 29.77
MOTA	2072 2073	C5/	CHS P		26.543	24.885	18.224	1.00 26.05
MOTA	2073	C48	CHS L		25.339	25.868	18.122	1.00 27.06
MOTA MOTA	2075	C50	CHS L	. 1	25.416	26.630	16.786	1.00 30.39 1.00 27.35
ATOM	2076	C38	CHS L	. 1	23.999	25.113	18.108 19.333	1.00 27.33
MOTA	2077	C35	CHS L	. 1	23.898	24.161 25.885	18.088	1.00 25.81
MOTA	2078	C29	CHS L	, 1 , 1	22.637 22.075	26.442	16.760	1.00 25.48
ATOM	2079	C25	CHS L	, 1	22.674	27.065	19.089	1.00 24.66
MOTA	2080 2081	C40	CHS I		21.683	24.733	18.480	1.00 24.66
ATOM ATOM	2082		CHS I		22.378	23.988	19.639	1.00 25.34 1.00 24.65
MOTA	2083	C18	CHS I	, 1	20.267	25.269	18.823 19.379	1.00 24.03
ATOM	2084	C15	CHS I	. 1	19.389	24.126 25.910	17.559	1.00 25.94
ATOM	2085		CHS I		19.656 20.616	26.987	16.956	1.00 25.70
ATOM	2086	C23	CHS I		18.195	26.423	17.788	1.00 25.96
MOTA	2087 2088		CHS I		18.216	27.828	18.461	1.00 23.41
MOTA MOTA	2089	C12	CHS I		17.391		18.627	1.00 27.66 1.00 27.52
MOTA	2090	C9	CHS I	. 1	15.878		18.705 19.343	1.00 27.32
MOTA	2091		CHS I		17.928	24.439 26.540	16.432	
MOTA	2092	C1	CHS I		17.457 15.966		16.596	1.00 25.61
MOTA	2093	C4 C7	CHS I		15.184	25.850	17.366	
MOTA	2094 2095	06	CHS		13.884	26.323		
MOTA MOTA		s1	CHS :	ւ 1	12.600			
ATOM		03	CHS :	L 1	11.492			
ATOM		02	CHS	L 1	12.386			
MOTA		04	CHS		12.791 34.374			1.00 24.18
ATOM		0	HOH T		13.751		14.717	1.00 25.05
MOTA			HOH		17.585	18.928	1.035	1.00 25.61
ATOM ATOM			HOH	V 4	19.468			
ATOM			HOH	V 5	28.242			
ATOM	2105	0	нон		26.219 25.424			1.00 29.16
ATOM			HOH		37.940			1.00 29.22
ATOM			НОН НОН		34.532	27.583	19.498	3 1.00 30.78
MOTA MOTA			нон		36.533	3 26.810	13.236	
ATOM			HOH	V 11	19.929	34.372	33.559	1.00 31.12

			30.464 36.924 16.913 1.00 32.33	0
MOTA	2111 0	HOH V 12	30.464 36.924 16.913 1.00 32.33 39.694 19.997 26.277 1.00 32.46	0
MOTA	2112 0	HOH V 13	10.618 25.915 9.224 1.00 33.09	0
MOTA	2113 0	HOH V 14	19 089 15 060 21.458 1.00 33.35	0
MOTA	2114 0	HOH V 15	19 982 38 502 24.574 1.00 33.56	0
ATOM	2115 0	HOH V 16	20 188 18 773 31.889 1.00 34.82	0
MOTA	2116 0	HOH V 17	22 916 26 367 25 939 1.00 35.28	0
ATOM	2117 0	HOH V 18	21 757 13 531 27 380 1.00 35.38	0
MOTA	2118 0	HOH V 19 HOH V 20	21 923 18 531 7.233 1.00 35.96	O
MOTA	2119 0		22 404 32 602 17.864 1.00 36.22	0
MOTA	2120 0		20 520 39 171 20 916 1.00 35./3	0
MOTA	2121 0	нон V 22 нон V 23	26.956 19.335 8.080 1.00 37.09	0
MOTA	2122 0	HOH V 24	17.942 26.092 21.769 1.00 37.19	0
ATOM	2123 0 2124 0	HOH V 25	30.129 36.843 14.123 1.00 37.60	0
ATOM	2124 0 2125 0	HOH V 26	26 979 35.078 38.228 1.00 37.66	0
MOTA	2126 0	HOH V 27	11.702 12.320 -11.449 1.00 37.83	Ö
MOTA	2127 0	HOH V 28	24.019 40.426 26.459 1.00 38.20	ŏ
ATOM ATOM	2128 0	HOH V 29	32.889 38.167 8.976 1.00 38.30	ŏ
ATOM	2129 0	HOH V 30	26.368 37.122 27.563 1.00 38.38 26.038 37.728 37.444 1.00 38.65	ŏ
MOTA	2130 0	HOH V 31	20.030 37.733	ŏ
MOTA	2131 0	HOH V 32	1 100 1 00 20 60	ō
ATOM	2132 0	HOH V 33	24.134 13.000	0
MOTA	2133 0	HOH V 34	17.220 20.00	0
ATOM	2134 0	HOH V 35	24.450 27.15	0
MOTA	2135 O	нон v 36	14.400 37.120 00 000 1 00 10 15	0
ATOM	2136 O	HOH V 37	38.590 23.562 23.909 1.00 40.15 20.064 26.866 31.634 1.00 40.16	0
MOTA	2137 0	HOH V 38	5 285 36 507 11.739 1.00 40.86	O
MOTA	2138 0	HOH V 39 HOH V 40	5 515 30 530 16 484 1.00 40.87	0
MOTA	2139 0	HOH V 41	24.115 12.660 27.541 1.00 40.92	0
MOTA	2140 O 2141 O	HOH V 42	23.756 5.602 14.704 1.00 41.1/	0
MOTA	2141 O 2142 O	HOH V 43	10.524 40.707 27.825 1.00 41.34	0
MOTA	2142 0	HOH V 44	26.115 7.036 20.648 1.00 41.58	ő
ATOM ATOM	2144 0	HOH V 45	22.909 14.371 0.739 1.00 41.86 22.901 12.389 26.816 1.00 42.12	ŏ
ATOM	2145 0	HOH V 46	JU1001 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Õ
ATOM	2146 O		27.030 30.323	0
ATOM	2147 O		27.520 30.22	0
MOTA	2148 O		19.208 17.322 27.275 1.00 42.36 17.702 22.996 26.002 1.00 42.43	0
MOTA	2149 0		21 518 40 403 26.071 1.00 42.44	0
MOTA	2150 0		29 008 37 276 26 773 1.00 42.97	O
MOTA			16 797 40 023 17.063 1.00 43.20	0
ATOM			27 959 18.192 30.078 1.00 43.25	0
ATOM			27.189 38.094 30.644 1.00 43.31	0
MOTA			32.853 5.119 27.654 1.00 43.36	ŏ
ATOM ATOM			25.498 15.066 28.345 1.00 43.59 26.277 3.798 24.349 1.00 43.69	ŏ
ATOM			20.277	ŏ
ATOM		нон V 59	22.22. 22. 22. 2. 2. 2. 2. 2. 2. 2. 2. 2	Ŏ
ATOM			1/0001	0
ATOM) HOH V 61	3.022 30.00	0
ATOM	2161 C		29.565 0.033 25.439 1.00 44.03 37.471 27.196 26.904 1.00 44.11	0
ATOM			14 114 35.615 19.648 1.00 44.14	Ō
ATOM			22 375 30 570 3.935 1.00 44.29	0
ATOM			22 67A 1A 801 -1.168 1.00 44.27	0
ATOM			10.607 41.218 4.126 1.00 44.59	0
ATOM		60	5.553 22.195 -4.232 1.00 45.31	0
MOTA		HOH V 69	18.683 8.716 -3.851 1.00 45.45	0
MOTA MOTA		нон v 70	31.216 36.554 23.614 1.00 45.65 32.042 38.382 12.898 1.00 45.78	ő
OTA		о нон v 71	32.042 30.302 == 1 00 45 05	ŏ
ATOM		о нон v 72	41.074 40.000	ŏ
ATON		O HOH V 73	24.525 ±0.720	0
ATOL	M 2173 (O HOH V 74	41 603 15 767 13.285 1.00 46.25	0
ATO		O HOH V 75	41.603 15.767 13.285 1.00 46.25 21.193 17.911 28.154 1.00 46.47	0
ATO	•	O HOH V 76 O HOH V 77	29.518 22.554 36.275 1.00 46.60	0
OTA	M 2176	о нон v 77		

MOTA	2177	0	HOH V 78	32.636			1.00 47.00	
ATOM	2178	ŏ	HOH V 79	13.479			1.00 47.13 1.00 47.21	
ATOM	2179	Õ	HOH V 80	32.129	25.488		1.00 47.21	
ATOM	2180	0	HOH V 81	5.317	15.523		1.00 47.24	
ATOM	2181	0	HOH V 82	14.590	12.994 -	.T3.T30	1.00 47.42	
ATOM	2182	0	HOH V 83	31.688	18.521	32.632	1.00 47.42	
ATOM	2183	0	HOH V 84	17.527	41.724	24.627	1.00 47.76	
ATOM	2184	0	HOH V 85	2.758	27.645	-6.136 9.361	1.00 47.77	
ATOM	2185	0	HOH V 86	39.479	15.402	7.716	1.00 47.80	
ATOM	2186	0	HOH V 87	27.097	39.457 38.493	18.833	1.00 48.18	
ATOM	2187	0	HOH A 88	14.854	28.965	31.902	1.00 48.22	
MOTA	2188	0	HOH V 89	16.442	18.094	16.102	1.00 48.28	
MOTA	2189	0	HOH V 90	6.592 25.862	43.114	20.667	1.00 48.28	
MOTA	2190	0	HOH V 91	25.820	31.283	38.083	1.00 48.37	
MOTA	2191	0	HOH V 92	21.448	8.215	-6.909	1.00 48.43	
MOTA	2192	0	HOH V 93 HOH V 94	30.315	7.953	13.447	1.00 48.47	
ATOM	2193	0		11.333	3.609	-1.448	1.00 48.50	
ATOM	2194	0	HOH V 95 HOH V 96	25.475	26.684	-3.988	1.00 48.54	
MOTA	2195	0	HOH V 97	21.825	7.068	6.249	1.00 48.57	
MOTA	2196 2197	0	HOH V 98	26.277	39.627	9.743	1.00 48.67	
MOTA MOTA	2198	ŏ	HOH V 99	10.637	33.053	31.840	1.00 48.70	
ATOM	2199	ŏ	HOH V 100	8.248	10.674	15.177	1.00 48.90	
ATOM	2200	ŏ	HOH V 101	5.925	25.750	18.970	1.00 48.97	
MOTA	2201	ō	HOH V 102	15.403	29.322	-7.859	1.00 49.09 1.00 49.16	
ATOM	2202	Ö	HOH V 103	3.536	35.057	9.239	1.00 49.10	
ATOM	2203	0	HOH V 104	24.615	19.046	6.759 32.348	1.00 49.22	
ATOM	2204	0	HOH V 105	26.458	22.354	8.558	1.00 49.24	
MOTA	2205	0	HOH V 106	29.329	9.438	25.260	1.00 49.30	
MOTA	2206	0	HOH V 107	38.968	26.081 31.078	20.463	1.00 49.55	
ATOM	2207	0	HOH V 108	33.166 23.661	41.348	9.046	1.00 49.57	
MOTA	2208	0	HOH V 109	-1.905	38.422	-2.103	1.00 49.58	
MOTA	2209	0	HOH V 110 HOH V 111	23.567	25.829	32.172	1.00 49.84	
MOTA	2210	0	HOH V 111 HOH V 112	39.174	28.173	18.167	1.00 49.89	
ATOM	2211	0	HOH V 112	6.546	17.330	-8.809	1.00 50.15	
MOTA	2212 2213	Ö	HOH V 114	15.378	36.610	16.329	1.00 50.24	
MOTA MOTA	2214	ŏ	HOH V 115	24.014	21.545	30.393	1.00 50.25	
ATOM	2215	ŏ	HOH V 116	13.119	40.412	25.848	1.00 50.51	
ATOM	2216	ŏ	HOH V 117	34.344	32.657	10.572	1.00 50.99 1.00 51.01	
ATOM	2217	Ō	HOH V 118	26.462	26.162	35.827	1.00 51.01	
ATOM	2218	0	HOH V 119	37.119	20.213	15.138	1.00 51.01	
MOTA	2219	0	HOH V 120	20.402	7.809	0.264 33.511	1.00 51.21	
MOTA	2220	0	HOH V 121	32.907	23.096	25.933	1.00 51.36	
MOTA	2221	0	HOH V 122	18.316 22.210	15.239 27.272	33.235	1.00 51.39	
MOTA	2222	0	HOH V 123	4 773	34.446	-7.751	1.00 51.56	
MOTA	2223	0	HOH V 124	-11.176		-12.026	1.00 51.70	
MOTA	2224	0	HOH V 125 HOH V 126	29.201		16.488	1.00 51.72	
MOTA	2225	0	HOH V 128	-14.169		-15.792	1.00 51.83	
MOTA	2226	0	HOH V 128	27.174		2.087	1.00 51.83	
ATOM	2227 2228	0	HOH V 129	12.661		30.244	1.00 51.89	
MOTA	2229		HOH V 130	16.175	21.212		1.00 51.93	
ATOM ATOM	2230		HOH V 131	20.211	40.398		1.00 52.00	
ATOM	2231		HOH V 132	-13.899	29.982		1.00 52.10	
MOTA	2232		HOH V 133	15.844	9.719		1.00 52.40 1.00 52.59	
MOTA	2233		нон V 134	31.386		17.146		
ATOM	2234		HOH V 135	0.640				
MOTA	2235		HOH V 136	42.270				
ATOM	2236		HOH V 137	17.490				
MOTA	2237		HOH V 138	29.839				
ATOM	2238		HOH V 139	4.290 19.892				
MOTA	2239		HOH V 140	9.212			1.00 53.10	
MOTA	2240		HOH V 141 HOH V 142	31.957		37.099	1.00 53.23	
MOTA	2241		HOH V 142	40.970			1.00 53.27	
MOTA	2242	. 0	11011 0 140					

WO 03/093312 PCT/EP03/04433

ATOM	2243	0	HOH V 144	40.782	22.485	20.153	1.00 53.41
ATOM	2244	0	HOH V 145	4.688 12.405	33.007 · 42.730	-12.475 -6.583	1.00 53.62 1.00 53.65
MOTA	2245	0	HOH V 146 HOH V 147	30.118	41.753	23.343	1.00 53.90
ATOM ATOM	2246 2247	0	HOH V 148	40.310	19.731	15.626	1.00 54.03
MOTA	2248	ŏ	HOH V 149	9.904		-10.125	1.00 54.05 1.00 54.10
MOTA	2249	0	HOH V 150	35.645 3.249	26.966 13.849	10.324 9.818	1.00 54.10
MOTA	2250 2251	0	HOH V 151 HOH V 152	3.249 8.994	41.917	8.500	1.00 54.13
MOTA MOTA	2251	Ö	HOH V 152	25.494	7.351	8.323	1.00 54.13
ATOM	2253	0	HOH V 154	-19.853	30.788	-6.983 26.243	1.00 54.14 1.00 54.20
ATOM	2254	0	HOH V 155 HOH V 156	28.190 14.754	2.825 37.385	13.109	1.00 54.20
MOTA MOTA	2255 2256	0	HOH V 150	13.944	9.467	-11.887	1.00 54.33
ATOM	2257	ŏ	HOH V 158	5.602	27.878	16.557	1.00 54.52 1.00 54.70
MOTA	2258	0	HOH V 159	35.605 24.308	5.102 35.094	13.754 -1.504	1.00 54.70
MOTA	2259 2260	0	HOH V 160 HOH V 161	28.337	18.154	4.417	1.00 54.85
ATOM ATOM	2261	ŏ	HOH V 162	34.895	34.791	30.514	1.00 54.94
ATOM	2262	0	HOH V 163	4.910	16.781	14.763 5.200	1.00 55.00 1.00 55.13
ATOM	2263	0	HOH V 164 HOH V 165	11.023 39.542	5.038 17.117	25.841	1.00 55.21
ATOM ATOM	2264 2265	ŏ	HOH V 166	24.386	37.780	-6.091	1.00 55.24
ATOM	2266	Ŏ	HOH V 167	20.889	19.941	29.200 -14.805	1.00 55.34 1.00 55.38
MOTA	2267	0	HOH V 168 HOH V 169	6.752 25.163	5.963	12.276	1.00 55.50
ATOM ATOM	2268 2269	0	HOH V 170	28.609	39.754	12.521	1.00 55.51
MOTA	2270	ŏ	HOH V 171	11.031	13.390	$14.244 \\ 2.257$	1.00 55.56 1.00 55.60
ATOM	2271	0	HOH V 172 HOH V 173	24.662 36.161	35.439 34.403	25.458	1.00 55.61
ATOM ATOM	2272 2273	0	HOH V 173	9.631	6.595	3.959	1.00 55.62
ATOM	2274	ŏ	HOH V 175	38.038	17.337	8.038	1.00 55.79 1.00 55.88
MOTA	2275	0	HOH V 176	0.83 <u>4</u> 30.977	36.938 6.285	9.105 15.282	1.00 55.88 1.00 55.89
ATOM ATOM	2276 2277	0	HOH V 177 HOH V 178	36.456	34.296	14.233	1.00 55.99
ATOM	2278	ŏ	HOH V 179	-16.740	27.510	-6.376	1.00 56.17 1.00 56.32
ATOM	2279	0	HOH V 180	17.830 27.092	28.498 42.066	-7.217 23.041	1.00 56.32 1.00 56.37
ATOM ATOM	2280 2281	0	HOH V 181 HOH V 182	32.854	20.918	3.041	1.00 56.40
ATOM	2282	ŏ	HOH V 183	33.531	36.555	20.279	1.00 56.52
MOTA	2283	0	HOH V 184	29.161 30.947	9.790 21.061	11.459 33.802	1.00 56.74 1.00 56.78
MOTA MOTA	2284 2285	0	HOH V 185 HOH V 186	4.419	10.917	12.329	1.00 57.20
ATOM	2286	ŏ	HOH V 187	35.731	21.349	33.562	1.00 57.25
MOTA	2287	0	HOH V 188	10.127	34.435 39.636	-7.921 5.433	1.00 57.31 1.00 57.31
ATOM ATOM	2288 2289	0	нон V 189 нон V 190	24.815 16.135	28.959	-10.450	1.00 57.40
ATOM	2290	ŏ	HOH V 191	28.755	27.074	-0.804	1.00 57.58 1.00 58.09
ATOM	2291	0	HOH V 192	37.694 12.094	28.335 17.839	20.845 22.662	1.00 58.09
MOTA MOTA	2292 2293	0	нон V 193 нон V 194	16.739	12.034	-12.326	1.00 58.15
ATOM	2294	ŏ	HOH V 195	35.658	34.834	39.271	1.00 58.17
MOTA	2295	0	нон V 196	6.325 40.239	23.731 32.219	-10.962 19.158	1.00 58.22 1.00 58.22
MOTA MOTA	2296 2297	0	HOH V 197 HOH V 198	42.009	17.600	28.618	1.00 58.40
ATOM	2298	ŏ	HOH V 199	13.977	43.767	4.977	1.00 58.43
MOTA	2299	0	HOH V 200	16.099	2.261 4.492	-8.711 15.572	1.00 58.43 1.00 58.44
ATOM ATOM	2300 2301	0	HOH V 201 HOH V 202	28.967 -9.860	29.231	-7.273	1.00 58.50
ATOM	2301	ő	HOH V 203	19.071	45.087	23.986	1.00 58.89
ATOM	2303	0	HOH V 204	23.529	32.968 19.843	-5.882 29.263	1.00 59.37 1.00 59.50
ATOM	2304 2305	0	HOH V 205 HOH V 206	42.799 21.137	24.412	31.357	1.00 59.65
ATOM ATOM	2305		HOH V 207	21.855	22.367	32.296	1.00 59.84
MOTA	2307	0	HOH V 208	3.008 25.290	31.149 39.928	11.774 29.735	1.00 59.88 1.00 59.89
ATOM	2308	0	HOH V 209	23.230	39.340	25.155	

		_	010	20 546	26.076	-5.981	1.00 60.27	0
MOTA	2309	0	HOH V 210	20.546		-0.636	1.00 60.32	ŏ
MOTA	2310	0	HOH V 211	7.922	7.232		1.00 60.32	ŏ
ATOM	2311	0	HOH V 212	7.268	35.864			0
MOTA	2312	0	HOH V 213	5.789		-10.740	1.00 60.43	
MOTA	2313	0	HOH V 214	26.552	14.136	-0.935	1.00 60.54	0
MOTA	2314	0	HOH V 215	41.103	32.645	22.002	1.00 60.87	0
ATOM	2315	0	HOH V 216	10.211	45.156	8.475	1.00 61.19	0
ATOM	2316	0	HOH V 217	25.176	9.626	5.053	1.00 61.26	0
ATOM	2317	0	HOH V 218	11.154	41.223	20.664	1.00 61.36	0
ATOM	2318	Ö	HOH V 219	12.673	39.495	16.829	1.00 61.48	0
ATOM	2319	ŏ	HOH V 220	6.931	21.130	20.882	1.00 61.81	0
ATOM	2320	ŏ	HOH V 221	34.324	35.314	27.782	1.00 61.99	0
ATOM	2321	ŏ	HOH V 222	22.533	27.773	-4.889	1.00 62.36	0
ATOM	2322	ŏ	HOH V 223	26.615	24.563	-3.514	1.00 62.43	0
	2323	ŏ	HOH V 224	22.620	8.612	-0.252	1.00 62.66	0
MOTA		ö	HOH V 225	7.850	40.686	5.273	1.00 62.89	0
ATOM	2324	Ö	HOH V 225	13.072	10.222	19.270	1.00 62.97	0
ATOM	2325	_	HOH V 227	36.863	23.365	8.281	1.00 63.29	0
ATOM	2326	0		3.086	21.555	0.662	1.00 63.45	Ō
ATOM	2327	0	HOH V 228	40.090	16.185	28.416	1.00 63.62	Ō
MOTA	2328	0	HOH V 229	28.499	41.692	20.652	1.00 63.74	Ö
MOTA	2329	0	HOH V 230		21.524	-0.933	1.00 63.76	Ö
ATOM	2330	0	HOH V 231	5.053	22.767	-9.711	1.00 63.86	ŏ
MOTA	2331	0	HOH V 232	18.279	13.207	14.475	1.00 64.13	ŏ
MOTA	2332	0	HOH V 233	4.021		18.023	1.00 64.17	ŏ
MOTA	2333	0	HOH V 234	20.707	46.785	-5.185	1.00 64.17	ŏ
MOTA	2334	0	HOH V 235	18.269	24.266			ŏ
MOTA	2335	0	HOH V 236	-1.075	31.083	6.459	1.00 64.71	ŏ
ATOM	2336	0	HOH V 237	36.067	6.771	10.766	1.00 64.72	0
ATOM .	2337	0	нон у 238	41.379	11.059	22.312	1.00 64.85	ő
MOTA	2338	0	HOH V 239	2.764	21.069	-4.139	1.00 64.89	0
ATOM	2339	0	HOH V 240	36.774	12.493	29.500	1.00 64.91	0
ATOM	2340	0	HOH V 241	33.576	7.054	15.865	1.00 65.14	0
ATOM	2341	0	HOH V 242	14.783	25.737	26.607	1.00 65.39	0
ATOM	2342	0	HOH V 243	19.632	29.934	-8.079	1.00 65.40	0
ATOM	2343	0	HOH V 244	19.893	42.353	12.315	1.00 65.64	0
ATOM	2344	O	HOH V 245	30.511	40.345	32.883	1.00 66.15	0
ATOM	2345	0	HOH V 246	6.494		-13.514	1.00 66.20	0
ATOM	2346	0	HOH V 247	41.592	29.824	26.952	1.00 67.14	0
ATOM	2347	0	HOH V 248	10.095	12.965	-13.010	1.00 68.08	0
ATOM	2348	Ó	HOH V 249	28.076	13.999	7.164	1.00 68.53	O
ATOM	2349	ō	HOH V 250	16.142	3.364	3.323	1.00 68.80	0
ATOM	2350	ō	HOH V 251	11.453	41.019	-1.487	1.00 68.99	O
ATOM	2351	ŏ	HOH V 252	22.049	30.697	36.943	1.00 69.14	0
ATOM	2352	ŏ	HOH V 253	31.306	29.631	39.320	1.00 69.25	0
ATOM	2353	ŏ	HOH V 254	26.120	35.578	0.298	1.00 69.34	0
ATOM	2354	ŏ	HOH V 255	37.240	33.402	37.433	1.00 69.56	0
ATOM	2355	ŏ	HOH V 256	14.450	19.763	22.059	1.00 70.09	0
T OLI	233	9						